

Sequence Listing

<110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.

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Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln
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His Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr
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35 40 45

Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
50 55 60

Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
65 70 75

Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
80 85 90

Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
95 100 105

Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
110 115 120

Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu
125 130 135

Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro
140 145 150

Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val
155 160 165

Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys
170 175 180

Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys
185 190 195

Ala	Phe	Gly	Val	His	Val	Ser	Cys	Ile	Glu	Pro	Gly	Leu	Phe	Lys	200	205	210
Thr	Asn	Leu	Ala	Asp	Pro	Val	Lys	Val	Ile	Glu	Lys	Lys	Leu	Ala	215	220	225
Ile	Trp	Glu	Gln	Leu	Ser	Pro	Asp	Ile	Lys	Gln	Gln	Tyr	Gly	Glu	230	235	240
Gly	Tyr	Ile	Glu	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Gly	Asn	Lys	Ser	245	250	255
Tyr	Val	Asn	Met	Asp	Leu	Ser	Pro	Val	Val	Glu	Cys	Met	Asp	His	260	265	270
Ala	Leu	Thr	Ser	Leu	Phe	Pro	Lys	Thr	His	Tyr	Ala	Ala	Gly	Lys	275	280	285
Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala	290	295	300
Leu	Gln	Asp	Phe	Leu	Leu	Leu	Lys	Gln	Lys	Ala	Glu	Leu	Ala	Asn	305	310	315
Pro Lys Ala Val																	

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapiens

<400> 11
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 gcccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150
 gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200
 atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250
 caactgtcga gattgcagcg gaatatgatt ctcttctctc ttgcctttct 300
 gcttttctgt ggactcctct totacatcaa cttggctgac cattggaaag 350
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400
 gggttaaaac cagcaaatac acccgtctta ccagctcctc agaaggcgga 450
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
 acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550
 ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagcccctgt 600
 ggatccccgc ccggaaggag atccgcagag gacagtcatc agctggaggg 650

gagcggatgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700
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 agtgcatctg aactatcgcc agaagggcgt gattgacgtc ttcttgcattg 800
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 cgcgctggac accatgtgga tcttgggtct gaggaagaa tttgaggaag 950
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 ttcagccgat tcacacgggt cccctcgggt ggctattctt ccatcaacaa 1950
 tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000
 tcttggggga gacgctcaag tatctgttct tgctcttctc cgatgacca 2050
 aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccaccctct 2100

gcctatctgg acccctgcct aggggtggatg gctgctggtg tggggacttc 2150
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 ctcagatgtc cccaatccaa gggctctggag gggctgccgt gactccagag 2550
 gcctgaggct ccagggtgg ctctggtgtt tacaagctgg actcagggat 2600
 cctcctggcc gccccgcagg gggcttggag ggctggacgg caagtccgtc 2650
 tagctcacgg gccctccag tggaatgggt cttttcgggt gagataaaag 2700
 ttgatttgct ctaaccgcaa 2720

<210> 12
 <211> 699
 <212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

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Gln	Ser	Asp	Phe	Leu	Thr	Pro	Pro	Val	Gly	Gly	Ala	Pro	Trp	Ala
				20					25				30	

Val	Ala	Thr	Thr	Val	Val	Met	Tyr	Pro	Pro	Pro	Pro	Pro	Pro	Pro
				35				40					45	

His	Arg	Asp	Phe	Ile	Ser	Val	Thr	Leu	Ser	Phe	Gly	Glu	Ser	Tyr
				50				55					60	

Asp	Asn	Ser	Lys	Ser	Trp	Arg	Arg	Arg	Ser	Cys	Trp	Arg	Lys	Trp
				65				70					75	

Lys	Gln	Leu	Ser	Arg	Leu	Gln	Arg	Asn	Met	Ile	Leu	Phe	Leu	Leu
				80				85					90	

Ala	Phe	Leu	Leu	Phe	Cys	Gly	Leu	Leu	Phe	Tyr	Ile	Asn	Leu	Ala
				95				100					105	

Asp His Trp Lys	Ala Leu Ala Phe Arg	Leu Glu Glu Glu Gln Lys	110	115	120
Met Arg Pro Glu	Ile Ala Gly Leu Lys	Pro Ala Asn Pro Pro Val	125	130	135
Leu Pro Ala Pro	Gln Lys Ala Asp Thr	Asp Pro Glu Asn Leu Pro	140	145	150
Glu Ile Ser Ser	Gln Lys Thr Gln Arg	His Ile Gln Arg Gly Pro	155	160	165
Pro His Leu Gln	Ile Arg Pro Pro Ser	Gln Asp Leu Lys Asp Gly	170	175	180
Thr Gln Glu Glu	Ala Thr Lys Arg Gln	Glu Ala Pro Val Asp Pro	185	190	195
Arg Pro Glu Gly	Asp Pro Gln Arg Thr	Val Ile Ser Trp Arg Gly	200	205	210
Ala Val Ile Glu	Pro Glu Gln Gly Thr	Glu Leu Pro Ser Arg Arg	215	220	225
Ala Glu Val Pro	Thr Lys Pro Pro Leu	Pro Pro Ala Arg Thr Gln	230	235	240
Gly Thr Pro Val	His Leu Asn Tyr Arg	Gln Lys Gly Val Ile Asp	245	250	255
Val Phe Leu His	Ala Trp Lys Gly Tyr	Arg Lys Phe Ala Trp Gly	260	265	270
His Asp Glu Leu	Lys Pro Val Ser Arg	Ser Phe Ser Glu Trp Phe	275	280	285
Gly Leu Gly Leu	Thr Leu Ile Asp Ala	Leu Asp Thr Met Trp Ile	290	295	300
Leu Gly Leu Arg	Lys Glu Phe Glu Glu	Ala Arg Lys Trp Val Ser	305	310	315
Lys Lys Leu His	Phe Glu Lys Asp Val	Asp Val Asn Leu Phe Glu	320	325	330
Ser Thr Ile Arg	Ile Leu Gly Gly Leu	Leu Ser Ala Tyr His Leu	335	340	345
Ser Gly Asp Ser	Leu Phe Leu Arg Lys	Ala Glu Asp Phe Gly Asn	350	355	360
Arg Leu Met Pro	Ala Phe Arg Thr Pro	Ser Lys Ile Pro Tyr Ser	365	370	375
Asp Val Asn Ile	Gly Thr Gly Val Ala	His Pro Pro Arg Trp Thr	380	385	390
Ser Asp Ser Thr	Val Ala Glu Val Thr	Ser Ile Gln Leu Glu Phe			

				395					400					405
Arg	Glu	Leu	Ser	Arg 410	Leu	Thr	Gly	Asp	Lys 415	Lys	Phe	Gln	Glu	Ala 420
Val	Glu	Lys	Val	Thr 425	Gln	His	Ile	His	Gly 430	Leu	Ser	Gly	Lys	Lys 435
Asp	Gly	Leu	Val	Pro 440	Met	Phe	Ile	Asn	Thr 445	His	Ser	Gly	Leu	Phe 450
Thr	His	Leu	Gly	Val 455	Phe	Thr	Leu	Gly	Ala 460	Arg	Ala	Asp	Ser	Tyr 465
Tyr	Glu	Tyr	Leu	Leu 470	Lys	Gln	Trp	Ile	Gln 475	Gly	Gly	Lys	Gln	Glu 480
Thr	Gln	Leu	Leu	Glu 485	Asp	Tyr	Val	Glu	Ala 490	Ile	Glu	Gly	Val	Arg 495
Thr	His	Leu	Leu	Arg 500	His	Ser	Glu	Pro	Ser 505	Lys	Leu	Thr	Phe	Val 510
Gly	Glu	Leu	Ala	His 515	Gly	Arg	Phe	Ser	Ala 520	Lys	Met	Asp	His	Leu 525
Val	Cys	Phe	Leu	Pro 530	Gly	Thr	Leu	Ala	Leu 535	Gly	Val	Tyr	His	Gly 540
Leu	Pro	Ala	Ser	His 545	Met	Glu	Leu	Ala	Gln 550	Glu	Leu	Met	Glu	Thr 555
Cys	Tyr	Gln	Met	Asn 560	Arg	Gln	Met	Glu	Thr 565	Gly	Leu	Ser	Pro	Glu 570
Ile	Val	His	Phe	Asn 575	Leu	Tyr	Pro	Gln	Pro 580	Gly	Arg	Arg	Asp	Val 585
Glu	Val	Lys	Pro	Ala 590	Asp	Arg	His	Asn	Leu 595	Leu	Arg	Pro	Glu	Thr 600
Val	Glu	Ser	Leu	Phe 605	Tyr	Leu	Tyr	Arg	Val 610	Thr	Gly	Asp	Arg	Lys 615
Tyr	Gln	Asp	Trp	Gly 620	Trp	Glu	Ile	Leu	Gln 625	Ser	Phe	Ser	Arg	Phe 630
Thr	Arg	Val	Pro	Ser 635	Gly	Gly	Tyr	Ser	Ser 640	Ile	Asn	Asn	Val	Gln 645
Asp	Pro	Gln	Lys	Pro 650	Glu	Pro	Arg	Asp	Lys 655	Met	Glu	Ser	Phe	Phe 660
Leu	Gly	Glu	Thr	Leu 665	Lys	Tyr	Leu	Phe	Leu 670	Leu	Phe	Ser	Asp	Asp 675
Pro	Asn	Leu	Leu	Ser 680	Leu	Asp	Ala	Tyr	Val 685	Phe	Asn	Thr	Glu	Ala 690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
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cccatgcgcc gccgcctctc cgcaogatgt tcccctcgcg gaggaagcg 100
gcgagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150
ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtc	g	g	g	g	a	c	a	a	g	g	g	c	a	g	g	a	c	a	c	c	c	g	t	g	c	c	t	g	300		
ccccccagag	c	c	g	c	c	c	c	c	c	t	g	a	g	c	a	c	t	g	g	g	a	a	a	g	a	c	g	c	a	350	
cccaccgcct	g	g	c	a	g	t	g	c	t	g	g	t	c	c	g	c	a	a	c	g	c	t	t	c	g	c	a	g	a	400	
ctggtcttcg	t	g	c	c	c	c	a	c	a	t	g	c	g	c	g	c	t	t	c	c	t	c	t	g	a	g	c	a	g	450	
gcaccacatc	t	a	c	g	t	g	c	t	c	a	a	c	a	g	g	t	g	g	a	c	c	a	c	t	t	c	a	g	g	500	
cagcgctcat	c	a	a	c	g	t	g	g	g	c	t	t	c	t	g	g	a	g	a	c	a	c	a	g	c	a	c	g	a	550	
attgccatgc	a	c	g	a	c	g	t	t	g	a	c	c	t	g	c	t	c	c	c	t	c	a	a	c	a	g	a	g	g	600	
tggctttcct	g	a	g	g	c	t	g	g	g	c	c	c	t	t	c	c	a	c	g	t	g	g	c	c	c	c	g	g	a	650	
ctctctacca	c	t	a	c	a	a	g	a	c	c	t	a	t	g	t	c	g	g	c	g	g	c	g	c	a	c	c	t	g	700	
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ccgcgaggac	g	a	c	g	a	g	t	t	c	t	a	c	c	g	g	c	g	c	a	t	a	a	g	g	g	a	g	c	t	800	
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catgacccag	c	c	t	g	g	c	g	g	a	a	g	a	g	g	g	a	c	c	a	g	a	a	a	a	a	a	a	a	a	900	
acaggagcag	t	t	c	a	a	g	g	t	g	a	c	a	g	g	g	a	g	g	g	a	g	g	c	c	t	g	a	a	g	950	
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attcagctga	g	c	t	g	g	a	t	g	g	a	c	a	g	t	g	a	g	g	a	g	c	c	t	g	t	a	c	c	t	1100	
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ggccgccaag	g	c	a	g	g	c	t	t	g	g	c	t	g	g	g	c	c	a	g	g	g	g	g	g	g	g	t	g	c	1250	
cgctgcttgc	c	a	t	g	c	a	c	a	g	t	g	a	t	c	a	g	a	g	a	g	a	g	g	c	t	g	g	g	t	1300	
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<210> 17
<211> 327
<212> PRT
<213> Homo sapiens
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<221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 19-25,65-71,247-253,285-291,303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17
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 20 25 30
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35 40 45
 Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
 50 55 60
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
 65 70 75
 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
 80 85 90
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
 95 100 105
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
 110 115 120
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
 125 130 135
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

				140						145					150
Glu	Ser	Ser	Asn	Ser	Thr	Asp	Tyr	Ile	Ala	Met	His	Asp	Val	Asp	
				155					160					165	
Leu	Leu	Pro	Leu	Asn	Glu	Glu	Leu	Asp	Tyr	Gly	Phe	Pro	Glu	Ala	
				170					175					180	
Gly	Pro	Phe	His	Val	Ala	Ser	Pro	Glu	Leu	His	Pro	Leu	Tyr	His	
				185					190					195	
Tyr	Lys	Thr	Tyr	Val	Gly	Gly	Ile	Leu	Leu	Leu	Ser	Lys	Gln	His	
				200					205					210	
Tyr	Arg	Leu	Cys	Asn	Gly	Met	Ser	Asn	Arg	Phe	Trp	Gly	Trp	Gly	
				215					220					225	
Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg	Arg	Ile	Lys	Gly	Ala	Gly	Leu	
				230					235					240	
Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr	Thr	Gly	Tyr	Lys	Thr	Phe	
				245					250					255	
Arg	His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys	Arg	Asp	Gln	Lys	Arg	
				260					265					270	
Ile	Ala	Ala	Gln	Lys	Gln	Glu	Gln	Phe	Lys	Val	Asp	Arg	Glu	Gly	
				275					280					285	
Gly	Leu	Asn	Thr	Val	Lys	Tyr	His	Val	Ala	Ser	Arg	Thr	Ala	Leu	
				290					295					300	
Ser	Val	Gly	Gly	Ala	Pro	Cys	Thr	Val	Leu	Asn	Ile	Met	Leu	Asp	
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Cys	Asp	Lys	Thr	Ala	Thr	Pro	Trp	Cys	Thr	Phe	Ser				
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<210> 18
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 18
 gcgaacgctt cgaggagtcc tgg 23

<210> 19
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-24
<223> Synthetic construct

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

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gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150
gattgggcct tctttccccc ttcttttctg tgtctcctgc ctcatcggcc 200
tgccatgacc tgcagccaag ccagccccg tggggaaggg gagaaagtgg 250
gggatggcta agaaagctgg gagatagggg acagaagagg gtagtgggtg 300
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
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<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
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<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

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20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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ggctccgggg cggcccgtta ggccagtgcg ccgccgctcg cccgcagggc 200

cccgcccgcc agcatggagc caccgggacg ccggcgggggc cgcgcgcagc 250

cgccgctggt gctgccgctc tcgctgttag cgctgctcgc gctgctggga 300

ggcggcgggc gcggcggcgc cgcggcgctg cccgccggct gcaagcacga 350

tgggcgggcc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400

tggtgtgcag cagcctggaa ctgcgcagg tcctgcccc agatactctg 450

cccaaccgca cggtcaccct gattctgagt aacaataaga tatccagct 500

gaagaatggc tcattttctg ggtaagtct ccttgaaaga ttggacctcc 550

gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600

tctctaaaaa gattgatct gacaaacaat cgaataggat gtctgaatgc 650

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<210> 24
 <211> 616
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-33
 <223> Signal peptide.

<220>
 <221> TRANSMEM
 <222> 13-40
 <223> Transmembrane domain (type II).

<400> 24
 Met Glu Pro Pro Gly Arg Arg Arg Gly Arg Ala Gln Pro Pro Leu
 1 5 10 15
 Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly
 20 25 30
 Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
 35 40 45
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
 50 55 60
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
 65 70 75
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
 80 85 90

<223> Synthetic construct

<400> 25

gaggactcac caatctgggtt cggc 24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

aactggaaag gaaggctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

gtaaaggaga agaacatcac ggtacgggat accaggtgtg tttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

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gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150
aaaaagaaaa cattcgtctt ttgggagAAC agattatTTT gactgagcaa 200
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ggaagggatg gatagtagca tccacctgag tagtctgac agtcggcatg 600
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<210> 29
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-21
 <223> Signal peptide.

<400> 29
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 Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp
 20 25 30
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
 50 55 60
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
 65 70 75
 Lys Gly Ser Gln Lys Ser
 80

<210> 30
 <211> 2128
 <212> DNA
 <213> Homo sapiens

<400> 30
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 caccaccatc acaaccacca cgacgtcatc ttcgggcctg gggcccccca 200
 tgatcgtggg gtcccctcgg gccctgacac agcccctggg tctccttcgc 250
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<210> 31
 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 31
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 Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val
 35 40 45
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
 50 55 60
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
 65 70 75
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
 80 85 90
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
 95 100 105
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
 110 115 120
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
 125 130 135
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
 140 145 150
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
 155 160 165
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
 170 175 180
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
 185 190 195
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
 200 205 210

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu
215 220 225

Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
230 235 240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu
245 250 255

Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln
260 265 270

Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr
275 280 285

Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr
290 295 300

Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala
305 310 315

His Leu Val Phe Val Lys Val
320

<210> 32
<211> 3680
<212> DNA
<213> Homo sapiens

<400> 32
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ctggccagcc tatgcatttt taagaaatta ttctgtatta ggtgctgtgc 200

taaacattgg gcactacagt gaccaaaca gactgaattc cccaagagcc 250

aaagaccagt gagggagacc aacaagaaac aggaaatgca aaagagacca 300

ttattactca ctatgactaa gggtcacaaa tggggtacgt tgatggagag 350

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taatataaaa atctttgtaa atctctaaaa 3680

<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

Met	Phe	Leu	Ala	Thr	Leu	Ser	Phe	Leu	Leu	Pro	Phe	Ala	His	Pro
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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
				20					25					30

Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45

His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60

Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75

Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90

Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105

Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120

Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
				125					130					135

Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
				140					145					150

Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
				155					160					165

Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
				170					175					180

Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
				185					190					195

His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
				200					205					210

Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
				215					220					225

Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
				230					235					240

Ala	Ser	Gln	Leu	Leu	Gly	Asp	Glu	Leu	Leu	Leu	Ala	Lys	Leu	Pro
			245						250					255
Pro	Ser	Arg	Glu	Ser	Ala	Phe	Arg	Ser	Leu	Gly	Pro	Leu	Glu	Ala
			260						265					270
Gln	Asp	Ser	Leu	Tyr	Asn	Ser	Pro	Leu	Thr	Glu	Ser	Cys	Leu	Ser
			275						280					285
Pro	Ala	Glu	Glu	Glu	Pro	Ala	Pro	Cys	Lys	Asp	Cys	Gln	Pro	Leu
			290						295					300
Cys	Pro	Pro	Leu	Thr	Gly	Ser	Trp	Glu	Arg	Gln	Arg	Gln	Ala	Ser
			305						310					315
Asp	Leu	Ala	Ser	Ser	Gly	Val	Val	Ser	Leu	Asp	Glu	Asp	Glu	Ala
			320						325					330
Glu	Pro	Glu	Glu	Gln										
				335										

<210> 34
 <211> 25
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct
 <400> 34
 tgtcctttgt cccagacttc tgtcc 25
 <210> 35
 <211> 50
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.
 <400> 35
 ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcatgct 50
 <210> 36
 <211> 25
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.
 <400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-23

<223> Synthetic construct.

<400> 37

ggcgagccct aactatccag gag 23

<210> 38

<211> 39

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-39

<223> Synthetic construct.

<400> 38

ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 39

ctgctgcaaa gcgagcctct tg 22

<210> 40

<211> 2084

<212> DNA

<213> Homo sapiens

<400> 40

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ccatctgttt tctctaatac acgacagatt cctttcagac aggacaactg 150

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<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

<400> 41
Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr
1 5 10 15
Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn
20 25 30
Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
35 40 45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
110 115 120
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
125 130 135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
140 145 150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
155 160 165
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
170 175 180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
185 190 195

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
				320					325					330
Arg	Thr	Ser	Val											

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
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 cccctaccgc cgtgcaaaag gaggaggcgc ggcaagacgt ggaggccctc 150
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
 tgccacccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250
 taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300
 tacaagtact tcatgcccac gagcaccatt taccgtggag agatgtgctt 350
 ttttgattct gaggatcctg caaatccct tcgtggagga gaggcctaact 400
 tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
 atcattgatg tgcctgtccc cagtttctct gatagtgacc ctgcagcaat 500
 tattcatgac tttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

ggaactgcta tctgatgcc ctaataactt ctattgttat gcctccaaaa 600
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ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu
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Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
20 25 30

Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
35 40 45

Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

	50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr	65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys	80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu	95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp	110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp	125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr	140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu	155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe	170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val	185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn	200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe	215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala	230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile	245	250	255
Val Glu Thr Lys Ile Cys Gln Glu	260		

<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
gggaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
caggatctcc tcttgagtc tgcagc 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgaac cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
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 gtttcggcgg cagccccag cctcctcatc cttctgttgc tgctgctggg 200
 gtctgtgcct gctaccgacg cccgctctgt gcccctgaag gccacgttcc 250
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 ggctccctgg cttttctgct gatgttcacg gtctgtgccg cggtcacac 500
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 agtcaggga catgggggtcc cagtggagac accagaggcg caggaggagc 850
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 tactttttta aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400
 aatactgtc ttaattttcc tgaagggtgg cccctgtttc tagttggtcc 1450
 aggattaggg atgtggggta tagggcattt aaatcctctc aagcgtctc 1500

caagcacccc cggcctgggg gtgagtttct catcccgcta ctgctgctgg 1550
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 gcacagctct ccagggtgctg agatataatg caccagcaca ataaaccttt 1900
 attccggcct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950
 aaaaaaaaaa aaaaaaaga 1969

<210> 50

<211> 283

<212> PRT

<213> Homo sapiens

<400> 50

Met	Val	Ser	Ala	Ala	Ala	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Leu	Gly	Ser	Val	Pro	Ala	Thr	Asp	Ala	Arg	Ser	Val	Pro	Leu	20	25	30	
Lys	Ala	Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	35	40	45	
Gly	Ser	Ser	Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro	50	55	60	
Ala	Leu	Ser	Pro	Thr	Ser	Met	Gly	Pro	Gln	Pro	Thr	Thr	Leu	Gly	65	70	75	
Gly	Pro	Ser	Pro	Pro	Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe	80	85	90	
Phe	Arg	Gln	Tyr	Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala	95	100	105	
Phe	Leu	Leu	Met	Phe	Ile	Val	Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln	110	115	120	
Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	Lys	Lys	125	130	135	
Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala	Gly	Gly	Pro	Arg	Ala	Phe	140	145	150	
Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Ala	155	160	165	

tccacggata ccccggaac tcagcaggca gctttggaat gaatcctcag 750
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 caacactcag ggagctgtgg ccagcctgg ctatggttca gtgagagcca 850
 gcaaccagaa tgaaggggtgc acgaatcccc caccatctgg ctcaggtgga 900
 ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtg 950
 cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
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 gaagcccgcg ggagcgggga atctgggatt cagggttca gaggacaggg 1250
 agtttccagc aacatgaggg aaataagcaa agagggaat cgcctccttg 1300
 gaggctctgg agacaattat cgggggcaag ggtcgagctg gggcagtgga 1350
 ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400
 tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450
 gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc 1500
 ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact 1550
 ccctccttaa aacaccaccc tctcatcact aatctcagcc ottgccccttg 1600
 aaataaacct tagctgcccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52
 <211> 440
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys
 1 5 10 15
 Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
 20 25 30
 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
 35 40 45
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

				50						55				60
Gly	Ala	Ala	Gly	Ser 65	Lys	Val	Ser	Glu	Ala 70	Leu	Gly	Gln	Gly	Thr 75
Arg	Glu	Ala	Val	Gly 80	Thr	Gly	Val	Arg	Gln 85	Val	Pro	Gly	Phe	Gly 90
Ala	Ala	Asp	Ala	Leu 95	Gly	Asn	Arg	Val	Gly 100	Glu	Ala	Ala	His	Ala 105
Leu	Gly	Asn	Thr	Gly 110	His	Glu	Ile	Gly	Arg 115	Gln	Ala	Glu	Asp	Val 120
Ile	Arg	His	Gly	Ala 125	Asp	Ala	Val	Arg	Gly 130	Ser	Trp	Gln	Gly	Val 135
Pro	Gly	His	Ser	Gly 140	Ala	Trp	Glu	Thr	Ser 145	Gly	Gly	His	Gly	Ile 150
Phe	Gly	Ser	Gln	Gly 155	Gly	Leu	Gly	Gly	Gln 160	Gly	Gln	Gly	Asn	Pro 165
Gly	Gly	Leu	Gly	Thr 170	Pro	Trp	Val	His	Gly 175	Tyr	Pro	Gly	Asn	Ser 180
Ala	Gly	Ser	Phe	Gly 185	Met	Asn	Pro	Gln	Gly 190	Ala	Pro	Trp	Gly	Gln 195
Gly	Gly	Asn	Gly	Gly 200	Pro	Pro	Asn	Phe	Gly 205	Thr	Asn	Thr	Gln	Gly 210
Ala	Val	Ala	Gln	Pro 215	Gly	Tyr	Gly	Ser	Val 220	Arg	Ala	Ser	Asn	Gln 225
Asn	Glu	Gly	Cys	Thr 230	Asn	Pro	Pro	Pro	Ser 235	Gly	Ser	Gly	Gly	Gly 240
Ser	Ser	Asn	Ser	Gly 245	Gly	Gly	Ser	Gly	Ser 250	Gln	Ser	Gly	Ser	Ser 255
Gly	Ser	Gly	Ser	Asn 260	Gly	Asp	Asn	Asn	Asn 265	Gly	Ser	Ser	Ser	Gly 270
Gly	Ser	Ser	Ser	Gly 275	Ser	Ser	Ser	Gly	Ser 280	Ser	Ser	Gly	Gly	Ser 285
Ser	Gly	Gly	Ser	Ser 290	Gly	Gly	Ser	Ser	Gly 295	Asn	Ser	Gly	Gly	Ser 300
Arg	Gly	Asp	Ser	Gly 305	Ser	Glu	Ser	Ser	Trp 310	Gly	Ser	Ser	Thr	Gly 315
Ser	Ser	Ser	Gly	Asn 320	His	Gly	Gly	Ser	Gly 325	Gly	Gly	Asn	Gly	His 330
Lys	Pro	Gly	Cys	Glu 335	Lys	Pro	Gly	Asn	Glu 340	Ala	Arg	Gly	Ser	Gly 345

Glu Ser Gly Ile	Gln Gly Phe Arg Gly	Gln Gly Val Ser Ser Asn	350	355	360
Met Arg Glu Ile	Ser Lys Glu Gly Asn Arg	Leu Leu Gly Gly Ser	365	370	375
Gly Asp Asn Tyr	Arg Gly Gln Gly Ser Ser	Trp Gly Ser Gly Gly	380	385	390
Gly Asp Ala Val	Gly Gly Val Asn Thr Val	Asn Ser Glu Thr Ser	395	400	405
Pro Gly Met Phe	Asn Phe Asp Thr Phe Trp	Lys Asn Phe Lys Ser	410	415	420
Lys Leu Gly Phe	Ile Asn Trp Asp Ala Ile	Asn Lys Asp Gln Arg	425	430	435
Ser Ser Arg Ile	Pro		440		

<210> 53
 <211> 3580
 <212> DNA
 <213> Homo sapiens

<400> 53
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 ctttgctgac catgttggtc ccttgctgga atattaccgg gacatcttca 150
 ctctcctgct ggcctgcac cggagcttgg tgttgctgca ggagagtgg 200
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<210> 54
<211> 280
<212> PRT
<213> Homo sapiens

<400> 54

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				20					25					30
Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
				35					40					45
His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
				50					55					60
Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
				65					70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
				80					85					90
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
				95					100					105
Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
				110					115					120
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
				125					130					135
Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
				140					145					150
Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu
				155					160					165
Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu
				170					175					180
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala
				185					190					195
Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg
				200					205					210
Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala
				215					220					225
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp
				230					235					240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
				245					250					255
Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala
				260					265					270
Arg	Gly	Glu	Arg	Arg	Gly	Cys	Ser	Arg	Ala					
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<210> 55
<211> 2401
<212> DNA
<213> Homo sapiens

<400> 55
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cgacacctac ccctcagcag acgccggaga gaaatgagta gcaacaaaga 200
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a 2401

<210> 56

<211> 299

<212> PRT

<213> Homo sapiens

<400> 56

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			20						25					30

Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg		35	40	45
Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro		50	55	60
Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val		65	70	75
Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro		80	85	90
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro		95	100	105
Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg		110	115	120
Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln		125	130	135
Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly		140	145	150
Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val		155	160	165
Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala		170	175	180
Val	Ser	Pro	Gly	Arg	Met	Arg	Gln	Phe	Asp	Asp	Leu	Phe	Arg	Gly		185	190	195
Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr		200	205	210
Gly	Trp	Phe	Thr	Met	Val	Ile	Ala	Val	Glu	Leu	Cys	Asp	His	Val		215	220	225
His	Val	Tyr	Gly	Met	Val	Pro	Pro	Asn	Tyr	Cys	Ser	Gln	Arg	Pro		230	235	240
Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro		245	250	255
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly		260	265	270
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp		275	280	285
Ala	Gln	Leu	Tyr	Gly	Ile	Thr	Phe	Ser	His	Pro	Ser	Trp	Thr			290	295	

<210> 57
 <211> 4277
 <212> DNA
 <213> Homo sapiens

<400> 57

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<210> 58
<211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

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				20					25					30	
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	
				35					40					45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	
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Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	
				65					70					75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	
				80					85					90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	
				95					100					105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	
				110					115					120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	
				125					130					135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	
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His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	
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Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	
				170					175					180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	
				185					190					195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	
				200					205					210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	
				215					220					225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	
				230					235					240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	
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Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	
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<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 59
gggaaacaca gcagtcattg cctgc 25

<210> 60
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 60
gcacacgtag cctgtcgctg gagc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-42
<223> Synthetic construct.

<400> 61
caccctaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
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<210> 63
<211> 487
<212> PRT
<213> Homo sapiens

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35 40 45

Pro Ser Ala Leu Thr Thr Pro Gly Leu Thr Thr Pro Gly Thr Pro
65 70 75

Phe Pro Leu Val Asp Gly His Asn Asp Leu Pro Gln Val Leu Arg
95 100 105

Ser His Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val
125 130 135

Gln Thr Ala Val Arg Leu Ala Leu Glu Gln Ile Asp Leu Ile His
155 160 165

Glu Gly Leu Asn Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val
185 190 195

Phe Tyr Val Leu Gly Val Arg Tyr Leu Thr Leu Thr Phe Thr Cys
215 220 225

Tyr Thr Asn Val Ser Gly Leu Thr Ser Phe Gly Glu Lys Val Val
245 250 255

71

ccttcacctg cagtacacca tgggc 25

<210> 65

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 65

gtcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-47

<223> Synthetic construct.

<400> 66

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<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

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gcccattgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350

agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400

atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450

gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500

acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550

tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaggtgc 600

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<210> 68
<211> 183
<212> PRT
<213> Homo sapiens

<400> 68
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Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
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Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
35 40 45
Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
50 55 60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu	65	70	75
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val	80	85	90
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr	95	100	105
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp	110	115	120
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala	125	130	135
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	140	145	150
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys	155	160	165
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys	170	175	180
Met Leu Ser																	

<210> 69
 <211> 3170
 <212> DNA
 <213> Homo sapiens

<400> 69
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<210> 70
<211> 259
<212> PRT
<213> Homo sapiens

<400> 70
Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu Leu
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Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser
20 25 30
Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
35 40 45

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aaaatacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350
ggatttgttc ttttatcccc cttttaaaagt catccgtcct tggctcagga 400
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gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550
ctcaagcccc caacatccca gtcctcagtc ctcagtcatc ttgacttcaa 600
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<210> 72
<211> 363
<212> PRT
<213> Homo sapiens

<400> 72
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Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
35 40 45
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
50 55 60
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
65 70 75
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
80 85 90
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
95 100 105
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
110 115 120
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
125 130 135
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
140 145 150
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
155 160 165
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
170 175 180
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
185 190 195
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
200 205 210
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
215 220 225

Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser
				275					280					285
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln
				290					295					300
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn
				305					310					315
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr
				320					325					330
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg
				335					340					345
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp
				350					355					360
Leu	Ile	Arg												

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 73
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<210> 74
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 74
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<210> 75
 <211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
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<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
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<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

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Gln	Ser	Ser	Ala	Val	Leu	Leu	His	Ser	Ala	Val	Glu	Glu	Thr	Asp
				20					25					30
Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu
				35					40					45
Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro
				50					55					60
Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val
				65					70					75

Ala Arg Gly Ala	Pro Ala Leu Leu Thr	Cys Val Asn Arg Gly His	80	85	90
Val Trp Thr Asp	Arg His Val Glu Glu	Ala Gln Gln Val Val His	95	100	105
Trp Asp Arg Gln	Pro Pro Gly Val Pro	His Asp Arg Ala Asp Arg	110	115	120
Leu Leu Asp Leu	Tyr Ala Ser Gly Glu	Arg Arg Ala Tyr Gly Pro	125	130	135
Leu Phe Leu Arg	Asp Arg Val Ala Val	Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe	Ser Leu Arg Ile Glu	Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr	Ser Cys His Leu His	His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg	Val Phe His Leu Thr	Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro	Arg Gly Ser Pro Gly	Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly	Pro Asp Pro Thr Leu	Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile	Val Pro Glu Ser Arg	Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val	Leu Ala Thr Leu Leu	Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu	Leu Ala Ala Arg Arg	Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln	Lys Ser Gly Lys Ser	Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe	Ala Val Ala Ala Gly	Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile	Gln Leu Asp Tyr Lys	Asn Asn Ile Leu Lys Glu	305	310	315
Arg Ala Glu Leu	Ala His Ser Pro Leu	Pro Ala Lys Tyr Ile Asp	320	325	330
Leu Asp Lys Gly	Phe Arg Lys Glu Asn	Cys Lys	335	340	

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

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<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser
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Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala
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Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
35 40 45

Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
50 55 60

Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
65 70 75

Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
80 85 90

Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
95 100 105

Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val
				110					115					120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val
				125					130					135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr
				140					145					150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe
				155					160					165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr
				170					175					180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met
				185					190					195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr
				200					205					210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp
				215					220					225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe
				230					235					240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu
				245					250					255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe
				260					265					270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser
				275					280					285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro
				290					295					300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val
				305					310					315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile
				320					325					330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe
				335					340					345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu
				350					355					360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn
				365					370					375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile
				380					385					390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys

	395		400		405
Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser					
	410		415		420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu					
	425		430		435
Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly					
	440		445		450
Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser					
	455		460		465
Ala Cys Ser Thr Leu Leu Val His Leu Ile					
	470		475		

<210> 80
 <211> 22
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

 <400> 80
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 <210> 81
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> 1-23
 <223> Synthetic construct.

 <400> 81
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 <210> 82
 <211> 49
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-49
 <223> Synthetic construct.

 <400> 82
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 <210> 83
 <211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

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<210> 84

<211> 567

<212> PRT

<213> Homo sapiens

<400> 84

Met	Ala	Pro	Leu	Ala	Leu	His	Leu	Leu	Val	Leu	Val	Pro	Ile	Leu
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Leu	Ser	Leu	Val	Ala	Ser	Gln	Asp	Trp	Lys	Ala	Glu	Arg	Ser	Gln
				20					25					30
Asp	Pro	Phe	Glu	Lys	Cys	Met	Gln	Asp	Pro	Asp	Tyr	Glu	Gln	Leu
				35					40					45
Leu	Lys	Val	Val	Thr	Trp	Gly	Leu	Asn	Arg	Thr	Leu	Lys	Pro	Gln
				50					55					60
Arg	Val	Ile	Val	Val	Gly	Ala	Gly	Val	Ala	Gly	Leu	Val	Ala	Ala
				65					70					75
Lys	Val	Leu	Ser	Asp	Ala	Gly	His	Lys	Val	Thr	Ile	Leu	Glu	Ala
				80					85					90
Asp	Asn	Arg	Ile	Gly	Gly	Arg	Ile	Phe	Thr	Tyr	Arg	Asp	Gln	Asn
				95					100					105
Thr	Gly	Trp	Ile	Gly	Glu	Leu	Gly	Ala	Met	Arg	Met	Pro	Ser	Ser
				110					115					120
His	Arg	Ile	Leu	His	Lys	Leu	Cys	Gln	Gly	Leu	Gly	Leu	Asn	Leu
				125					130					135
Thr	Lys	Phe	Thr	Gln	Tyr	Asp	Lys	Asn	Thr	Trp	Thr	Glu	Val	His
				140					145					150
Glu	Val	Lys	Leu	Arg	Asn	Tyr	Val	Val	Glu	Lys	Val	Pro	Glu	Lys
				155					160					165

Leu Gly Tyr Ala	Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu	170	175	180
Asp Ile Tyr Gln	Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys	185	190	195
Ala Leu Gly Cys	Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr	200	205	210
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala	215	220	225
Val Gln Leu Leu	Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr	230	235	240
Leu Ser Phe Ala	Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp	245	250	255
Arg Leu Gln Tyr	Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro	260	265	270
Arg Ala Leu Leu	Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala	275	280	285
Pro Val Val Ala	Met Thr Gln Gly Pro His Asp Val His Val Gln	290	295	300
Ile Glu Thr Ser	Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala	305	310	315
Asp Val Val Leu	Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile	320	325	330
Thr Phe Ser Pro	Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg	335	340	345
Arg Leu His Tyr	Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg	350	355	360
Arg Pro Phe Trp	Arg Glu Glu His Ile Glu Gly Gly His Ser Asn	365	370	375
Thr Asp Arg Pro	Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu	380	385	390
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala	395	400	405
Ala Phe Ala Gly	Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu	410	415	420
Asp Asp Val Ala	Ala Leu His Gly Pro Val Val Arg Gln Leu Trp	425	430	435
Asp Gly Thr Gly	Val Val Lys Arg Trp Ala Glu Asp Gln His Ser	440	445	450
Gln Gly Gly Phe	Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu			

	455		460		465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly					
	470		475		480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys					
	485		490		495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro					
	500		505		510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu					
	515		520		525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp					
	530		535		540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu					
	545		550		555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His					
	560		565		

<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
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 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200
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<210> 86
 <211> 739
 <212> PRT
 <213> Homo sapiens

<400> 86
 Met Asp Ala Leu Lys Pro Pro Cys Leu Trp Arg Asn His Glu Arg
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 Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro
 20 25 30

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His	Gln	Asn	Ile	Val	Ser	Asn	Ala	Ala	Ala	Phe	Leu	Lys	Cys	Val
				335					340					345
Glu	His	Ala	Tyr	Glu	Pro	Thr	Pro	Asp	Asp	Val	Ala	Ile	Ser	Tyr
				350					355					360
Leu	Pro	Leu	Ala	His	Met	Phe	Glu	Arg	Ile	Val	Gln	Ala	Val	Val
				365					370					375
Tyr	Ser	Cys	Gly	Ala	Arg	Val	Gly	Phe	Phe	Gln	Gly	Asp	Ile	Arg
				380					385					390
Leu	Leu	Ala	Asp	Asp	Met	Lys	Thr	Leu	Lys	Pro	Thr	Leu	Phe	Pro
				395					400					405
Ala	Val	Pro	Arg	Leu	Leu	Asn	Arg	Ile	Tyr	Asp	Lys	Val	Gln	Asn
				410					415					420
Glu	Ala	Lys	Thr	Pro	Leu	Lys	Lys	Phe	Leu	Leu	Lys	Leu	Ala	Val
				425					430					435
Ser	Ser	Lys	Phe	Lys	Glu	Leu	Gln	Lys	Gly	Ile	Ile	Arg	His	Asp
				440					445					450
Ser	Phe	Trp	Asp	Lys	Leu	Ile	Phe	Ala	Lys	Ile	Gln	Asp	Ser	Leu
				455					460					465
Gly	Gly	Arg	Val	Arg	Val	Ile	Val	Thr	Gly	Ala	Ala	Pro	Met	Ser
				470					475					480
Thr	Ser	Val	Met	Thr	Phe	Phe	Arg	Ala	Ala	Met	Gly	Cys	Gln	Val
				485					490					495
Tyr	Glu	Ala	Tyr	Gly	Gln	Thr	Glu	Cys	Thr	Gly	Gly	Cys	Thr	Phe
				500					505					510
Thr	Leu	Pro	Gly	Asp	Trp	Thr	Ser	Gly	His	Val	Gly	Val	Pro	Leu
				515					520					525
Ala	Cys	Asn	Tyr	Val	Lys	Leu	Glu	Asp	Val	Ala	Asp	Met	Asn	Tyr
				530					535					540
Phe	Thr	Val	Asn	Asn	Glu	Gly	Glu	Val	Cys	Ile	Lys	Gly	Thr	Asn
				545					550					555
Val	Phe	Lys	Gly	Tyr	Leu	Lys	Asp	Pro	Glu	Lys	Thr	Gln	Glu	Ala
				560					565					570
Leu	Asp	Ser	Asp	Gly	Trp	Leu	His	Thr	Gly	Asp	Ile	Gly	Arg	Trp
				575					580					585
Leu	Pro	Asn	Gly	Thr	Leu	Lys	Ile	Ile	Asp	Arg	Lys	Lys	Asn	Ile
				590					595					600
Phe	Lys	Leu	Ala	Gln	Gly	Glu	Tyr	Ile	Ala	Pro	Glu	Lys	Ile	Glu
				605					610					615

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<210> 88

<211> 660

<212> PRT

<213> Homo sapiens

<400> 88

Met	Asp	Asp	Trp	Lys	Pro	Ser	Pro	Leu	Ile	Lys	Pro	Phe	Gly	Ala
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Arg	Lys	Lys	Arg	Ser	Trp	Tyr	Leu	Thr	Trp	Lys	Tyr	Lys	Leu	Thr
				20					25					30
Asn	Gln	Arg	Ala	Leu	Arg	Arg	Phe	Cys	Gln	Thr	Gly	Ala	Val	Leu
				35					40					45
Phe	Leu	Leu	Val	Thr	Val	Ile	Val	Asn	Ile	Lys	Leu	Ile	Leu	Asp
				50					55					60
Thr	Arg	Arg	Ala	Ile	Ser	Glu	Ala	Asn	Glu	Asp	Pro	Glu	Pro	Glu
				65					70					75
Gln	Asp	Tyr	Asp	Glu	Ala	Leu	Gly	Arg	Leu	Glu	Pro	Pro	Arg	Arg
				80					85					90
Arg	Gly	Ser	Gly	Pro	Arg	Arg	Val	Leu	Asp	Val	Glu	Val	Tyr	Ser
				95					100					105
Ser	Arg	Ser	Lys	Val	Tyr	Val	Ala	Val	Asp	Gly	Thr	Thr	Val	Leu
				110					115					120
Glu	Asp	Glu	Ala	Arg	Glu	Gln	Gly	Arg	Gly	Ile	His	Val	Ile	Val
				125					130					135

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val	380	385	390
Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe	395	400	405
Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr	410	415	420
Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu			

425					430					435				
Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly
			440						445					450
Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys
			455						460					465
Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg
			470						475					480
Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val
			485						490					495
Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly
			500						505					510
Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val
			515						520					525
Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala
			530						535					540
Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu
			545						550					555
Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr
			560						565					570
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp
			575						580					585
Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp
			590						595					600
Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe
			605						610					615
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro
			620						625					630
Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu
			635						640					645
Pro	Pro	Pro	Lys	Glu	Glu	Gly	Ala	Pro	Gly	Ala	Pro	Glu	Gln	Thr
			650						655					660

<210> 89

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89

gatggcaaaa cgtgtgtttg acacg 25

<210> 90
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 90
cctcaaccag gccacgggcc ac 22

<210> 91
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 91
cccaggcaga gatgcagtac aggc 24

<210> 92
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 92
cctccagtag gtggatggat tggctc 26

<210> 93
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 93
ctcacctcat gaggatgagg ccatggtgct attcctcaac atggtag 47

<210> 94
<211> 3037
<212> DNA
<213> Homo sapiens

<400> 94

cggacgcgtg ggctgctggt gggaaggcct aaagaactgg aaagcccact 50
ctcttggaac caccacacct gtttaaagaa cctaagcacc atttaaagcc 100
actggaaatt tggtgtctag tggttggtgg tgaataaagg agggcagaat 150
ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 200
gttacgtggc cggaatcatt cccttggtg ttaatttctc agaggaacga 250
ctgaagctgg tgactgtttt ggggtgctggc cttctctgtg gaactgctct 300
ggcagtcacg gtgcctgaag gagtacatgc cctttatgaa gatattcttg 350
agggaaaaca ccaccaagca agtgaaacac ataatgtgat tgcacagac 400
aaagcagcag aaaaatcagt tgtccatgaa catgagcaca gccacgacca 450
cacacagctg catgcctata ttggtgtttc cctcgttctg ggcttcgttt 500
tcatgttgct ggtggaccag attggttaact cccatgtgca ttctactgac 550
gatccagaag cagcaaggtc tagcaattcc aaaatcacca ccacgctggg 600
tctggttgtc catgctgcag ctgatggtgt tgctttggga gcagcagcat 650
ctacttcaca gaccagtgtc cagttaattg tgtttggtgg aatcatgcta 700
cataaggcac cagctgcttt tggactggtt tccttcttga tgcacgctgg 750
cttagagcgg aatcgaatca gaaagcactt gctggtcttt gcattggcag 800
caccagttat gtccatggtg acatacttag gactgagtaa gagcagtaaa 850
gaagcccttt cagaggtgaa cgccacggga gtggccatgc ttttctctgc 900
cgggacattt ctttatgttg ccacagtaca tgtcctccct gaggtgggag 950
gaatagggca cagccacaag cccgatgcca cgggaggag aggcctcagc 1000
cgcctggaag tggcagccct ggttctgggt tgcctcatcc ctctcatcct 1050
gtcagtagga caccagcatt aaatgttcaa ggtccagcct tgggtccagg 1100
ccgtttgcca tccagtgaga acagccggca cgtgacagct actcaattcc 1150
tcagtctctt gtctcacctt gcgcatctct acatgtattc ctagagtcca 1200
gaggggaggt gaggttaaaa cctgagtaat ggaaaagctt ttagagtaga 1250
aacacattta cgttgcagtt agctatagac atcccattgt gttatctttt 1300
aaaaggccct tgacattttg cgttttaata tttctcttaa ccctattctc 1350
agggagatg gaatttagtt ttaaggaaaa gaggagaact tcatactcac 1400
aatgaaatag tgattatgaa aatacagtgt tctgtaatta agctatgtct 1450

ctttcttctt agtttagagg ctctgctact ttatccattg atttttaaca 1500
 tgggtcccac catgtaagac tggtgcttta gcatctatgc cacatgogtt 1550
 gatggaaggt catagcacc cactacttag atgctaaagg tgattctagt 1600
 taatctggga ttagggctcag gaaaatgata gcaagacaca ttgaaagctc 1650
 tctttatact caaaagagat atccattgaa aagggatgtc tagagggatt 1700
 taaacagctc ctttggcacg tgcctctctg aatccagcct gccattccat 1750
 caaatggagc aggagaggtg ggaggagctt ctaaagaggt gactggtatt 1800
 ttgtagcatt ccttgtcaag ttctcctttg cagaatacct gtctccacat 1850
 tcctagagag gagccaagtt ctagtagttt cagttctagg ctttccttca 1900
 agaacagtca gatcacaag tgtctttgga aattaaggga tattaaattt 1950
 taagtgattt ttggatgggt attgatatct ttgtagtagc tttttttaa 2000
 agactaccaa aatgtatggt tgtccttttt ttttgttttt ttttttttta 2050
 attatttctc ttagcagatc agcaatccct ctagggacct aaatactagg 2100
 tcagctttgg cgacactgtg tcttctcaca taaccacctg tagcaagatg 2150
 gatcataaat gagaagtgtt tgcctattga tttaaagctt attggaatca 2200
 tgtctcttgt ctcttcgtct tttctttgct tttcttctaa cttttccctc 2250
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 gtgggatgaa ttcttatcag gacaaccact tctcgaactg taataatgaa 2350
 gataataata tctttattct ttatcccctt caaagaaatt accttttgtgt 2400
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 ttaacagact aggataattt tttttcata tttgccaaaa ttttgtaaa 2550
 ccctgtcttg tcaaataagt gtataatatt gtattattaa tttattttta 2600
 ctttctatac catttcaaaa cacattacac taagggggaa ccaagactag 2650
 tttcttcagg gcagtggacg tagtagtttg taaaaacgtt ttctatgacg 2700
 cataagctag catgcctatg atttatttcc ttcatgaatt tgtcactgga 2750
 tcagcagctg tggaaataaa gcttgtagc cctctgctgg ccacagtgag 2800
 gaaagtagca caaataggat acagttgtat gtagtcattg gcaacaattg 2850
 catacaattt tactaccaag agaaggtata gtatggaaag tccaaatgac 2900

ttccttgatt ggatgttaac agctgactgg tgtgagactt gaggtttcat 2950
 ctagtccttc aaaactatat ggttgcctag attctctctg gaaactgact 3000
 ttgtcaaata aatagcagat tgtagtgtca aaaaaaa 3037

<210> 95
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 95
 Met Asp Asp Phe Ile Ser Ile Ser Leu Leu Ser Leu Ala Met Leu
 1 5 10 15
 Val Gly Cys Tyr Val Ala Gly Ile Ile Pro Leu Ala Val Asn Phe
 20 25 30
 Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu
 35 40 45
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
 50 55 60
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
 65 70 75
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
 80 85 90
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
 95 100 105
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
 110 115 120
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
 125 130 135
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
 140 145 150
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
 155 160 165
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
 170 175 180
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
 185 190 195
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
 200 205 210
 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
 215 220 225
 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

	230		235		240									
Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu
	245								250					255
Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly
	260								265					270
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg
	275								280					285
Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile
	290								295					300
Leu	Ser	Val	Gly	His	Gln	His								
				305										

<210> 96
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 96
 gttgtgggtg aataaaggag ggcag 25

<210> 97
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 97
 ctgtgctcat gttcatggac aactg 25

<210> 98
 <211> 50
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 98
 ggatgatttc atctccatta gcctgctgctc tctggctatg ttggtgggat 50

 <210> 99
 <211> 1429

<212> DNA
<213> Homo sapiens

<400> 99

gctcgaggcc ggccggcgcc ggagagcgac ccgggcggcc tcgtagcggg 50
gccccggatc cccgagtggc ggccggagcc tcgaaaagag attctcagcg 100
ctgatTTTga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150
ccgcccctcg tgctggccgc cctggtggcc tgcattcatcg tcttgggctt 200
caactactgg attgagagct cccggagcgt ggacctccag acacggatca 250
tgagagctgga aggcagggtc cgcaggcgcc ctgcagagag aggcgccgtg 300
gagctgaaga agaacgagtt ccaggagag ctggagaagc agcgggagca 350
gcttgacaaa atccagtcca gccacaactt ccagctggag agcgtcaaca 400
agctgtacca ggacgaaaag gcggttttgg tgaataacat caccacaggt 450
gagaggctca tccgagtgtc gcaagaccag ttaaagacct tgcagaggaa 500
ttacggcagg ctgcagcagg atgtcctcca gtttcagaag aaccagacca 550
acctggagag gaagttctcc tacgacctga gccagtgcatt caatcagatg 600
aaggaggtga aggaacagtg tgaggagcga atagaagagg tcaccaaaaa 650
ggggaatgaa gctgtagctt ccagagacct gaggtaaac aacgaccaga 700
gacagcagct ccaagccctc agtgagcctc agcccaggct gcaggcagca 750
ggcctgccac acacagaggt gccacaaggg aagggaacg tgcttggtaa 800
cagcaagtcc cagacaccag ccccagttc cgaagtgggt ttggattcaa 850
agagacaagt tgagaaagag gaaaccaatg agatccaggt ggtgaatgag 900
gagcctcaga gggacaggct gccgcaggag ccaggccggg agcagggtgt 950
ggaagacaga cctgtaggtg gaagaggctt cgggggagcc ggagaactgg 1000
gccagacccc acagggtcag gctgccctgt cagttagcca ggaaaatcca 1050
gagatggagg gccctgagcg agaccagctt gtcattcccc acggacagga 1100
ggaggagcag gaagctgccg gggaaggag aaaccagcag aaactgagag 1150
gagaagatga ctacaacatg gatgaaaatg aagcagaatc tgagacagac 1200
aagcaagcag ccctggcagg gaatgacaga aacatagatg tttttaatgt 1250
tgaagatcag aaaagagaca ccataaattt acttgatcag cgtgaaaagc 1300
ggaatcatat actctgaatt gaactggaat cacatatctt acaacagggc 1350

cgaagagatg actataaaat gttcatgagg gactgaatac tgaaaactgt 1400
 gaaatgtact aaataaaatg tacatctga 1429

<210> 100
 <211> 401
 <212> PRT
 <213> Homo sapiens

<400> 100
 Met Met Gly Leu Gly Asn Gly Arg Arg Ser Met Lys Ser Pro Pro
 1 5 10 15
 Leu Val Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe
 20 25 30
 Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg
 35 40 45
 Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg
 50 55 60
 Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu
 65 70 75
 Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe
 80 85 90
 Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val
 95 100 105
 Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu
 110 115 120
 Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln
 125 130 135
 Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg
 140 145 150
 Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu
 155 160 165
 Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys
 170 175 180
 Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp
 185 190 195
 Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu
 200 205 210
 Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly
 215 220 225
 Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser
 230 235 240

gctgacatct aggacttcat tattctataa ttcaggacca cagtggagta 3450
 tgatccctaa ctcttgattt ggatgcatct gagggacaag gggggcggtc 3500
 tccgaagtgg aataaaatag gccgggcgtg gtgacttgca cctataatcc 3550
 cagcactttg ggaggcagag gtgggaggat tgcttgggcc caggagttca 3600
 agaccagcct gtggaacata acaagacccc gtctctacta tttaaaaaaa 3650
 agtgtaataa aatgataata t 3671

<210> 102
 <211> 1089
 <212> PRT
 <213> Homo sapiens

<400> 102
 Met Gln Lys Ala Ser Val Leu Leu Phe Leu Ala Trp Val Cys Phe
 1 5 10 15
 Leu Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu
 20 25 30
 Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro
 35 40 45
 Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala
 50 55 60
 Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile
 65 70 75
 Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val
 80 85 90
 Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser
 95 100 105
 Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu
 110 115 120
 Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu
 125 130 135
 Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly
 140 145 150
 Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys
 155 160 165
 Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp
 170 175 180
 Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe
 185 190 195
 Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

	200	205	210
Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp	Asp
	215	220	225
Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His	Lys
	230	235	240
His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln	Met
	245	250	255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp	Thr
	260	265	270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly	Asp
	275	280	285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe	Leu
	290	295	300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu	Pro
	305	310	315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu	Leu
	320	325	330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met	Ala
	335	340	345
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser	Ala
	350	355	360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val	Ser
	365	370	375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln	Ala
	380	385	390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser	Ala
	395	400	405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala	Thr
	410	415	420
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly	Ala
	425	430	435
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val	Arg
	440	445	450
Met Ala Gly Gly	Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile	Cys
	455	460	465
Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe	Cys
	470	475	480
Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala	Ile
	485	490	495

Ala Tyr Ala Gly	Leu Leu Gly Thr Ile	Glu Leu Lys Leu Asp	Leu
500		505	510
Val Leu Leu Gly	Ala Val Ala Ala Val	Ser Ser Phe Leu Pro	Phe
515		520	525
Leu Trp Lys Ala	Trp Ala Gly Trp Gly	Ser Lys Arg Pro Leu	Ala
530		535	540
Thr Leu Phe Pro	Ile Pro Gly Pro Val	Leu Leu Leu Leu Leu	Phe
545		550	555
Arg Leu Ala Val	Phe Phe Ser Asp Ser	Phe Val Val Ala Glu	Ala
560		565	570
Arg Ala Thr Pro	Phe Leu Leu Gly Ser	Phe Ile Leu Leu Leu	Val
575		580	585
Val Gln Leu His	Trp Glu Gly Gln Leu	Leu Pro Pro Lys Leu	Leu
590		595	600
Thr Met Pro Arg	Leu Gly Thr Ser Ala	Thr Thr Asn Pro Pro	Arg
605		610	615
His Asn Gly Ala	Tyr Ala Leu Arg Leu	Gly Ile Gly Leu Leu	Leu
620		625	630
Cys Thr Arg Leu	Ala Gly Leu Phe His	Arg Cys Pro Glu Glu	Thr
635		640	645
Pro Val Cys His	Ser Ser Pro Trp Leu	Ser Pro Leu Ala Ser	Met
650		655	660
Val Gly Gly Arg	Ala Lys Asn Leu Trp	Tyr Gly Ala Cys Val	Ala
665		670	675
Ala Leu Val Ala	Leu Leu Ala Ala Val	Arg Leu Trp Leu Arg	Arg
680		685	690
Tyr Gly Asn Leu	Lys Ser Pro Glu Pro	Pro Met Leu Phe Val	Arg
695		700	705
Trp Gly Leu Pro	Leu Met Ala Leu Gly	Thr Ala Ala Tyr Trp	Ala
710		715	720
Leu Ala Ser Gly	Ala Asp Glu Ala Pro	Pro Arg Leu Arg Val	Leu
725		730	735
Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly	Leu
740		745	750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr	Val
755		760	765
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val	Leu
770		775	780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser	Gln Ala Asp Leu Asp	Tyr

785										790					795				
Val	Val	Pro	Gln	Ile	Tyr	Arg	His	Met	Gln	Gln	Glu	Glu	Phe	Arg	Gly				
				800					805						810				
Arg	Leu	Glu	Arg	Thr	Lys	Ser	Gln	Gly	Pro	Leu	Thr	Val	Ala	Ala					
				815					820					825					
Tyr	Gln	Leu	Gly	Ser	Val	Tyr	Ser	Ala	Ala	Met	Val	Thr	Ala	Leu					
				830					835					840					
Thr	Leu	Leu	Ala	Phe	Pro	Leu	Leu	Leu	Leu	His	Ala	Glu	Arg	Ile					
				845					850					855					
Ser	Leu	Val	Phe	Leu	Leu	Leu	Phe	Leu	Gln	Ser	Phe	Leu	Leu	Leu					
				860					865					870					
His	Leu	Leu	Ala	Ala	Gly	Ile	Pro	Val	Thr	Thr	Pro	Gly	Pro	Phe					
				875					880					885					
Thr	Val	Pro	Trp	Gln	Ala	Val	Ser	Ala	Trp	Ala	Leu	Met	Ala	Thr					
				890					895					900					
Gln	Thr	Phe	Tyr	Ser	Thr	Gly	His	Gln	Pro	Val	Phe	Pro	Ala	Ile					
				905					910					915					
His	Trp	His	Ala	Ala	Phe	Val	Gly	Phe	Pro	Glu	Gly	His	Gly	Ser					
				920					925					930					
Cys	Thr	Trp	Leu	Pro	Ala	Leu	Leu	Val	Gly	Ala	Asn	Thr	Phe	Ala					
				935					940					945					
Ser	His	Leu	Leu	Phe	Ala	Val	Gly	Cys	Pro	Leu	Leu	Leu	Leu	Trp					
				950					955					960					
Pro	Phe	Leu	Cys	Glu	Ser	Gln	Gly	Leu	Arg	Lys	Arg	Gln	Gln	Pro					
				965					970					975					
Pro	Gly	Asn	Glu	Ala	Asp	Ala	Arg	Val	Arg	Pro	Glu	Glu	Glu	Glu					
				980					985					990					
Glu	Pro	Leu	Met	Glu	Met	Arg	Leu	Arg	Asp	Ala	Pro	Gln	His	Phe					
				995					1000					1005					
Tyr	Ala	Ala	Leu	Leu	Gln	Leu	Gly	Leu	Lys	Tyr	Leu	Phe	Ile	Leu					
				1010					1015					1020					
Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu	Ala	Ala	Ser	Ile	Leu	Arg					
				1025					1030					1035					
Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe	Ala	Pro	Lys	Phe	Ile	Phe					
				1040					1045					1050					
Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser	Val	Gly	Leu	Leu	Leu	Gly					
				1055					1060					1065					
Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly	Ala	Val	Ser	Ser	Trp	Phe					
				1070					1075					1080					

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 103
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gcagttccct gtgtctctgg tggtttcct aaacctgcaa acatcacctt 100
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgctc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatacaaac agaacgtggt ccagtggtg gaccaaccac acgctgggtg 400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450
gtcccagggc cccctcgccg tgtcagcct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
aaaaaatcgt gattaacttt atcaccctca atatctogga tgattctaaa 750
atttctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800
ccttaatgat cctcagccca gcgggaacct gagggccct caggaggaag 850
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtcctt 950
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcggt 1100
ggcagtcttg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc 1150
aagacttaga cccctggcg caggagcaca cagactcgga ggagggggccg 1200
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250

gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300
 agccttctga gggggatggg ctcgagagg agggctcttct atctagactc 1350
 tatgaggagc cggtccaga caggccacca ggagaaaatg aaacctatct 1400
 catgcaattc atggaggaat ggggggttata tgtgcagatg gaaaactgat 1450
 gccaacactt ccttttgcct tttgtttcct gtgcaaaca gtgagtcacc 1500
 cctttgatcc cagccataaa gtacctggga tgaaagaagt tttttccagt 1550
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 cgtgtgtgat tggttcatgc atgtaggtct cttacaatg atgggtgggc 1650
 tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcaat 1700
 aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ser	Tyr	Asn	Gly	Leu	His	Gln	Arg	Val	Phe	Lys	Glu	Leu	Lys
1				5					10					15
Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20					25					30
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35					40					45
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55					60
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70					75
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85					90
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
				95					100					105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
				110					115					120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
				125					130					135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
				140					145					150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
				155					160					165

Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	170	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	185	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	200	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	215	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	230	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	245	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	260	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	275	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	290	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	305	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	320	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	335	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	350	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	365	375
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser	380	390
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly	395	405
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro	410	420
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly	425	435
Leu	Tyr	Val	Gln	Met	Glu	Asn									440	

<210> 105

<222> 1-51
<223> Synthetic construct.

<400> 109
ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacaat 50
c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
cggaacgctg ggccgacgag tgggcggacg cgtgggtctc tgcggggaga 50
cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100
tctgctgact gtggccaacc ccctgatgct gcccgtaag cccccgcag 150
gctcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200
aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250
cttcctgctg cgagcccgtt ggggtggtct gcccgccac tgcttcagcc 300
acagagacct ccgcaactgg ctggtggtgc tgggcgcca cgtcctgagt 350
actgcggagc ccaccagca ggtgtttggc atcgatgct tcaccacgca 400
ccccgactac caccatga cccacgcaa cgacatctgc ctgctgcggc 450
tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggtgcca 500
gggagaaggg ccaggcccc cacagcggg acacggtgcc ggggtgctgg 550
ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600
ccaagggtcc agtgctggac ccggacgtct gcaacagctc ctggaagggc 650
cacctgacac ttaccatgct ctgcacccgc agtggggaca gccacagacg 700
gggcttctgc tcggccgact ccggagggcc cctggtgtgc aggaaccggg 750
ctcagggcct cgtttccttc tcgggcctct ggtgcggcga cccaagacc 800
ccagacgtgt acacgcagg gtccgccttt gtggcctgga tctgggacgt 850
ggttcggcgg agcagtcacc agcccgccc cctgcctggg accaccaggc 900
ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950
gccgtccag gcctggaatg ttccgtggct gggcccccac ggaagcctga 1000
tggtcagggg tgggggtggg cgggcagcgg tggggcacac ccattccaca 1050
tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met	Gly	Leu	Gly	Leu	Arg	Gly	Trp	Gly	Arg	Pro	Leu	Leu	Thr	Val
1				5					10					15
Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp
				20					25					30
Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
				35					40					45
Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
				50					55					60
Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys
				65					70					75
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
				80					85					90
His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
				95					100					105
Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala
				110					115					120
Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly
				125					130					135
Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
				140					145					150
Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
				155					160					165
Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
				170					175					180
Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
				185					190					195
Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg
				200					205					210
Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
				215					220					225
Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
				230					235					240
Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
				245					250					255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
 260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
 275 280

<210> 112
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 112
 gacgtctgca acagctcctg gaag 24

<210> 113
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 113
 cgagaaggaa acgaggccgt gag 23

<210> 114
 <211> 44
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-44
 <223> Synthetic construct.

<400> 114
 tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115
 <211> 1808
 <212> DNA
 <213> Homo sapiens

<400> 115
 gagctaccca ggcggctggt gtgcagcaag ctccgcgcgcg actccggacg 50
 cctgacgcct gacgcctgtc cccggcccgc catgagccgc tacctgctgc 100
 cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150
 tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200

ggtcatcgtg acgggcgcca acacaggcat cgggaagcag accgccttgg 250
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300
 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
 tgtcaacgcc cggcacctgg acttggettcc cctcaagtct atccgagagt 400
 ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaataaac 450
 aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500
 gatgcagttt ggcgttaacc acctgggtca ctttctcttg acaaacttgc 550
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 gacgaggaag tataacacca aagccgccta ctgccagagc aagctcgcca 700
 tcgtcctctt caccaaggag ctgagccggc ggctgcaagg ctctggtgtg 750
 actgtcaacg ccctgcaccc cggcgtggcc aggacagagc tgggcagaca 800
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 ggaggctttg ggctgaaagt gccgcctgg tgggcttaga ggctccctct 1050
 gtgagggagc agccccctcc cagataacct ctggagcaga tttgaaagcc 1100
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 ctggcactac ctgagccggg agaccagga ctggcggccg ccatgcccgc 1200
 agtaggttct agggggcggt gctggccgca gtggactggc ctgcaggtga 1250
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 gcctgtcggg gagggttcca aggtgctccg tgaagagcat gggcaagtgg 1450
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 gtcctctctg agccttggtt tcttcagcag tgagatgctc agaataactg 1550
 ctgtctccca tgatgggtgtg gtacagcgag ctgttgctg gctatggcat 1600
 ggctgtgccc ggggtgtttg ctgagggtt cctgtgccag agcccagcca 1650

gagagcaggt gcaggtgtca tcccaggttc aggctctgca cggcatggag 1700
 tgggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750
 caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800
 gctcattt 1808

<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116
 Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala
 1 5 10 15
 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
 20 25 30
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
 110 115 120
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 140 145 150
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
 200 205 210
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
 215 220 225

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His	230	235	240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro	245	250	255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro	260	265	270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly	275	280	285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala	290	295	300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg	305	310	315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro	320	325	330

Arg

<210> 117
 <211> 2249
 <212> DNA
 <213> Homo sapiens

<400> 117
 gaagttcgcg agcgctggca tgtggtcctg gggcgcggtt ggcggtcgtg 50
 ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgctgctcg 100
 gggcgacacg ttctcgggcg tgaccagcgt ggcgcgcgcc ctggcgcccg 150
 agcgccggct gctggggctg ctgaggcgtt acctgcgcgg ggaggaggcg 200
 cggctgcggg acctgaactag attctacgac aaggtacttt ctttgcattg 250
 ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
 gagaacatcc gagctctgaa ggatggctat gagaagggtg agcaagacct 400
 tccagccttt gaggaccttg agggagcagc aagggccctg atgcggctgc 450
 aggacgtgta catgctcaat gtgaaaggcc tggcccaggg tgtctttcag 500
 agagtcaactg gctctgccat cactgacctg tacagcccca aacggctctt 550
 ttctctcaca ggggatgact gcttccaagt tggcaagggt gcctatgaca 600
 tgggggatta ttaccatgcc attccatggc tggaggaggc tgtcagtctc 650
 ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700

agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgttt 750
 cgtgtgccct cagcctctct cgggagtttc ttctctacag ccagataat 800
 aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850
 cccaaccac gtggttagctg aggctgtcat ccagaggccc aatatacccc 900
 acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950
 cagcccactc tctaccagat ccctagcctc tactgttcct atgagaccaa 1000
 ttccaacgcc tacctgctgc tccagcccat ccggaaggag gtcattccacc 1050
 tggagcccta cattgctctc taccatgact tcgtcagtga ctgagaggct 1100
 cagaaaatta gagaacttgc agaaccatgg ctacagaggc cagtgggtggc 1150
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200
 ggctgaagga cactgttgac ccaaaactgg tgaccctcaa ccaccgcatt 1250
 gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac ttgaccatg 1350
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 gcaacattta tgatctatct gagctcgggtg gaagctggag gagccacagc 1450
 cttcatctat gccaacctca gcgtgcctgt ggttaggaat gcagcactgt 1500
 tttggtggaa cctgcacagg agtgggtgaag gggacagtga cacacttcat 1550
 gctggctgtc ctgtcctggt gggagataag tgggtggcca acaagtggat 1600
 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650
 actgaaactgt tggcagagag aagctggtgg agtcctgtgg ctttccagag 1700
 aagccaggag ccaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750
 ctggaagaag gccttgtcag ctttgtctgt gcctcgcaa tcagaggcaa 1800
 gggagagggt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850
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 ggctgagag ggaagtttct ggagttcaga tactctctgt tgggaacagg 1950
 acatctcaac agtctcaggc togatcagtg ggtcttttgg cactttgaac 2000
 cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050
 tagcctgact ccagaactt taagacttcc tccccactgc cttctgctgc 2100
 agcccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150

tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

Gly	Asn	Val	Ser	Cys 245	Ala	Leu	Ser	Leu	Ser	Arg	Glu	Phe	Leu	Leu 255
Tyr	Ser	Pro	Asp	Asn 260	Lys	Arg	Met	Ala	Arg	Asn	Val	Leu	Lys	Tyr 270
Glu	Arg	Leu	Leu	Ala 275	Glu	Ser	Pro	Asn	His	Val	Val	Ala	Glu	Ala 285
Val	Ile	Gln	Arg	Pro 290	Asn	Ile	Pro	His	Leu	Gln	Thr	Arg	Asp	Thr 300
Tyr	Glu	Gly	Leu	Cys 305	Gln	Thr	Leu	Gly	Ser	Gln	Pro	Thr	Leu	Tyr 315
Gln	Ile	Pro	Ser	Leu 320	Tyr	Cys	Ser	Tyr	Glu	Thr	Asn	Ser	Asn	Ala 330
Tyr	Leu	Leu	Leu	Gln 335	Pro	Ile	Arg	Lys	Glu	Val	Ile	His	Leu	Glu 345
Pro	Tyr	Ile	Ala	Leu 350	Tyr	His	Asp	Phe	Val	Ser	Asp	Ser	Glu	Ala 360
Gln	Lys	Ile	Arg	Glu 365	Leu	Ala	Glu	Pro	Trp	Leu	Gln	Arg	Ser	Val 375
Val	Ala	Ser	Gly	Glu 380	Lys	Gln	Leu	Gln	Val	Glu	Tyr	Arg	Ile	Ser 390
Lys	Ser	Ala	Trp	Leu 395	Lys	Asp	Thr	Val	Asp	Pro	Lys	Leu	Val	Thr 405
Leu	Asn	His	Arg	Ile 410	Ala	Ala	Leu	Thr	Gly	Leu	Asp	Val	Arg	Pro 420
Pro	Tyr	Ala	Glu	Tyr 425	Leu	Gln	Val	Val	Asn	Tyr	Gly	Ile	Gly	Gly 435
His	Tyr	Glu	Pro	His 440	Phe	Asp	His	Ala	Thr	Ser	Pro	Ser	Ser	Pro 450
Leu	Tyr	Arg	Met	Lys 455	Ser	Gly	Asn	Arg	Val	Ala	Thr	Phe	Met	Ile 465
Tyr	Leu	Ser	Ser	Val 470	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr 480
Ala	Asn	Leu	Ser	Val 485	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp 495
Trp	Asn	Leu	His	Arg 500	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His 510
Ala	Gly	Cys	Pro	Val 515	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys 525
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser

530

535

540

Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 119

cgggacagga gaccagaaa ggg 23

<210> 120

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 120

ggccaagtga tccaaggcat cttc 24

<210> 121

<211> 49

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-49

<223> Synthetic construct.

<400> 121

ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens

<400> 122

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gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150

ggagagcccc ggagcccccg taaccgcgc ggggagcgc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250
gctcaagttt tcacttatca totattccac cgtgttctgg ctgattgggg 300
ccctggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatcctcct 400
gggcgctcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450
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tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700
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 catgttttgt tttgttttta аааааааа 1778

<210> 123
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 123
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 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
 20 25 30
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
 35 40 45
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
 50 55 60
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met
 65 70 75
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
 80 85 90
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
 95 100 105
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
 110 115 120
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
 125 130 135
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
 140 145 150
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
 155 160 165
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
 170 175 180
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
 185 190 195
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
 200 205 210
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
 215 220 225
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

<400> 127

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ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150
tgcagttctc atcctcggcc caaaagtcat caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
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acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400
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cattgaccgt ctggagtttg accttctgta tcctgccatc aagggtgaca 800
ccattcagct ctacctgggg gccaaagtgt tggactcaca gggaaagggtg 850
accaagtggg tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900
caacatcccg ttcagcctca tcgtgagtca ggacgtgggtg aaagctgcag 950
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aggacactcc cgagtttttt atagaccaag gccatgcaa ggtggcccaa 1150
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atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400
gatctgggggt ccagtgatca ttggtgaagg ccttgggatt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttggtg cttactccag cctccttggtg 1500
gaaacccagc tctcctgtct cccagtgaag acttggtatgg cagccatcag 1550
ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600
cctctctgca atcaataaac acttgcctgt gaaaaa 1636

<210> 128
<211> 484
<212> PRT
<213> Homo sapiens

<400> 128

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala	1	5	10	15
Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile	20	25	30	
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys	35	40	45	
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser	50	55	60	
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser	65	70	75	
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile	80	85	90	
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp	95	100	105	
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe	110	115	120	
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr	125	130	135	
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro	140	145	150	
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu	155	160	165	
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu	170	175	180	
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu	185	190	195	
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly	200	205	210	
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu	215	220	225	

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys
230 235 240

Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser
245 250 255

Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu
260 265 270

Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser
275 280 285

Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu
290 295 300

Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His
305 310 315

Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp
320 325 330

Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr
335 340 345

Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu
350 355 360

Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu
365 370 375

Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr
380 385 390

Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp
395 400 405

Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp
410 415 420

Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu
425 430 435

Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu
440 445 450

Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys
455 460 465

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
470 475 480

Pro Val Ser Gln

<210> 129
<211> 2213
<212> DNA
<213> Homo sapiens

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136

tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150
 cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200
 cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250
 aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300
 ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
 caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
 ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450
 atggatggat gtcatggaga ggcattggta ccgaacacag aaatttgga 500
 aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
 tggacaagag atgttgcttt cttactcaga caagaaggca ggcccatggg 600
 taatcttatc cgtaacagga ctaaagtcag agtgatggaa agggattggc 650
 agaatacaga caaagcagta aactgggtta gaaaggaagc aattaattac 700
 actgaaccat ttgttattta cttgggatta aatttaccac acccttacc 750
 ttcaccatct tctggagaaa attttggtat ttcaacattt cacacatctc 800
 tttattggct tgaaaaagtg tctcatgatg ccatcaaat cccaaagtgg 850
 tcacctttgt cagaaatgca ccctgtagat tattactctt cttatacaaa 900
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 tttattatgc tatgtgtgct gagacagatg ccatgcttgg tgaaattatt 1000
 ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050
 ctcagaccat ggagagctgg ccatggaaca tcgacagttt tataaaatga 1100
 gcatgtacga ggctagtgc catgttccgc ttttgatgat gggaccagga 1150
 attaaagccg gcctacaagt atcaaagtgt gtttctcttg tggatattta 1200
 ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagt 1250
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 gtcaaaaacc tgcattccac ctggattctg agtgaattcc atggatgtaa 1350
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 gatccagatg aattaacaaa tgttgctgta aaatttccag aaattactta 1500
 ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys		
380	385	390
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser		
395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg		
410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile		
425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr		
440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln		
455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val		
470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile		
485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln		
500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln		
515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val		
530	535	

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
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 ctacatccta ggctttctgg ggcttttggg cacactgggt gccatgctgc 200
 tccccagctg gaaaacaagt ttttatgtcg gtgccagcat tgtgacagca 250
 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
 catcaccag tgtgacatct atagaccct tctgggcctg cccgctgaca 350
 tccaggctgc ccaggccatg atgggtgacat ccagtgaat ctctccctg 400
 gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atcccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500
 ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggata 550
 ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600
 tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650
 ctggaatcat cctctgcttt tctgtctcat cccagagaaa tcgctccaac 700
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 gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800
 cagggtatgt gtgaagaacc aggggccaga gctgggggggt ggctgggtct 850
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 attgccaagg atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050
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 gcagcctggg acatttaaaa aaata 1475

<210> 134
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 134
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
 1 5 10 15
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 20 25 30
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
 35 40 45
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400
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 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
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 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
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 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
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 gtcttttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100
 agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

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 agaactgcga ctacagcccg acctcggatg acaggctttg tcgcagtgtc 350
 agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagt 450
 gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
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 ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600
 ggactctgaa ccctcctgat gaccctatg gccaacatca acccggcacc 650
 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700
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 tatgtacttt ataaatgaaa a 771

<210> 138

<211> 110

<212> PRT

<213> Homo sapiens.

<400> 138

Met	Ala	Pro	Arg	Gly	Cys	Ile	Val	Ala	Val	Phe	Ala	Ile	Phe	Cys
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Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met
			20					25						30
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp
			35					40						45
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val
			50					55						60
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg
			65					70						75
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu
			80					85						90
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu
			95					100						105
Cys	Arg	Ser	Val	Ser										
			110											

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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 ctccccggca ccagaagtgc ctctgcggt cgcagggcga catgggctc 150
 cccacggccc tggaggccgg cagctgggcg tggggatccc tgctcttcgc 200
 tctcttcctg gctgcgtccc taggtccggg ggcagccttc aaggtcgcca 250
 cgccgtattc cctgtatgtc tgtcccagg ggcagaacgt caccctcacc 300
 tgcaggctct tgggccctgt ggacaaaggg cacgatgtga cttctacaa 350
 gacgtggtac cgcagctcga ggggcgagg gcagacctgc tcagagcgcc 400
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 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500
 gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550
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 ttcaagggat tgaanaaaaa ggctttgaag cctcaccacc tgcccagggg 900
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 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400
 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450

Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu
				155					160					165
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val
				170					175					180
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala
				185					190					195
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu
				200					205					210
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg
				215					220					225
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile
				230					235					240
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro
				245					250					255
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln
				260					265					270
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro
				275					280					285
Leu	Ser	Pro	Pro	Gly	Pro	Gly	Asp	Val	Phe	Phe	Pro	Ser	Leu	Asp
				290					295					300
Pro	Val	Pro	Asp	Ser	Pro	Asn	Phe	Glu	Val	Ile				
				305					310					

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 cttagacctc ccttctgccc ctcttttctt gccaccgct gcttctggtc 150
 ccttctccga ccccgtctta gcagcagacc tcctgggggtc tgtgggttga 200
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250
 ccgctcccg accagcgccc tgacctggg gaaaggatgg ttcccaggt 300
 gaggtcctc tcctccttgc tgggactgc gctgctctgg ttccccctgg 350
 actccacgc tcgagccgc ccagacatgt tctgcctttt ccatgggaag 400
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gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500
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cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600
ggccccacca aagtccctgcc agcacaacgg gacctgtac caacacggag 650
agatcttcag tgcccatgag ctgttccct cccgcctgcc caaccagtgt 700
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750
ccccgaacca ggctgcccag caccctccc actgccagac tcctgctgcc 800
aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850
cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900
tgggagaaaag agaggcccg gacccccagc cccactggc ctcagcgccc 950
ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050
cgggaagacg tactcccacg gggaggtgtg gcaccgggcc ttccgtgcct 1100
tcggccccctt gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150
tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa 1200
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gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
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ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
<211> 451
<212> PRT
<213> Homo sapiens
<400> 142

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 gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550
 ttttaaggctcc gcaaggcggg ccaggggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
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 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
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 ttgaggggaa gaggctgact gtacgttcct tctactctgg caccactctc 100
 caggctgcca tggggcccag caccctctc ctcattctgt tccttttgtc 150
 atggctcgga cccctccaag gacagcagca ccaccttggt gagtacatgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
 actgctggag gtggcagaga aggagcggga ggcaactcaga actgaggccg 350
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp
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Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met
20 25 30

Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln
35 40 45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn
50 55 60

Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala
65 70 75

Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu
80 85 90

Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro
95 100 105

Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys
110 115 120

Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys
125 130 135

Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg
140 145 150

Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln
155 160 165

Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala
170 175 180

Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala
185 190 195

Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr
200 205 210

Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro
215 220 225

Pro Gly Arg Pro Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln
230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser
245 250 255

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 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
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aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148

Met	Ala	Leu	Met	Leu	Ser	Leu	Val	Leu	Ser	Leu	Leu	Lys	Leu	Gly	1	5	10	15
Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala	20	25	30	
Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys	35	40	45	
Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe	50	55	60	
Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe	65	70	75	
Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp	80	85	90	
Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr	95	100	105	
Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser	110	115	120	
Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly	125	130	135	
Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile	140	145	150	
Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala	155	160	165	
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg	170	175	180	
Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu	185	190	195	
Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His	200	205	210	
Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp	215	220	225	
Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu				

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgccca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccggtggc ggtggcgccg gcggttgccg aggcttcctt 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggag 150
gcctcgccct gttgtgctgc gcgcgcgcgc ccgccgccgt cgcctcagcc 200
gcctcggcgc ggaatgtcac cggcggcgcc ggggcgcgcg ggcaggtgga 250
cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300
gggcgacggc tcccaaggcc caggccccga ggaccgggac cccgcgcgcc 350
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tgttttaaga acttttagct ccttgacaaa gaagtgcttt atacttttagc 1900
 actaaatatt ttaaagtctt tataaatgat attatactgt tatggaatat 1950
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000
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 tgaggccagg agttctagat gagcctggcc agcacagtga aaccccgctc 2100
 ctactaaaaa tacaacaaa ttagctgggc gtggtggcac acacctgtag 2150
 tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200
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 agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys	1	5	10	15
Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn	20	25	30	
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro	35	40	45	
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala	50	55	60	
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala	65	70	75	
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro	80	85	90	
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr	95	100	105	
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala	110	115	120	
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro	125	130	135	
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val	140	145	150	
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro	155	160	165	
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro				

	170	175	180
Ala Thr Glu Ala Pro Ser Ser Pro Pro Pro Glu Tyr Val Cys Asn	185	190	195
Cys Ser Val Val Gly Ser Leu Asn Val Asn Arg Cys Asn Gln Thr	200	205	210
Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr Gln Gly Leu His Cys	215	220	225
Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu	230	235	240
Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro	245	250	255
Cys Asn Arg			

<210> 154
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 154
 aactgctctg tgggttggaag cctg 24

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 155
 cagtccatg gctgacagac ccac 24

<210> 156
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-38
 <223> Synthetic construct.

<400> 156
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
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 ttctggcttt ggtctcggtg cccagggccccc aggcctgctg gttgggaaga 100
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggcggcctc 150
 ccgggaaaag ggctttgccg tggagaagga catgaagaac gtcgtggggg 200
 tgggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
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 gggccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
 1 5 10 15
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
				155					160					

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

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aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50
gctgctgctg cccctgctct gggggaggga gagggcggaa ggacagacaa 100
gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggccctgtgt 150
gtccatgtgc cctgctcctt ctctacccc tcgcatggct ggatttaccc 200
tggcccagta gttcatggct actggttccg ggaaggggcc aatacagacc 250
aggatgctcc agtggccaca aacaacccag ctcgggcagt gtgggaggag 300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
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gtgagcaggg gacacccoct atgatctcct ggataggac ctccgtgtcc 600
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gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
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cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
tggtctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900
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Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu
				125					130					135
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile
				140					145					150
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser
				155					160					165
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp
				170					175					180
Ile	Gly	Thr	Ser	Val	Ser	Pro	Leu	Asp	Pro	Ser	Thr	Thr	Arg	Ser
				185					190					195
Ser	Val	Leu	Thr	Leu	Ile	Pro	Gln	Pro	Gln	Asp	His	Gly	Thr	Ser
				200					205					210
Leu	Thr	Cys	Gln	Val	Thr	Phe	Pro	Gly	Ala	Ser	Val	Thr	Thr	Asn
				215					220					225
Lys	Thr	Val	His	Leu	Asn	Val	Ser	Tyr	Pro	Pro	Gln	Asn	Leu	Thr
				230					235					240
Met	Thr	Val	Phe	Gln	Gly	Asp	Gly	Thr	Val	Ser	Thr	Val	Leu	Gly
				245					250					255
Asn	Gly	Ser	Ser	Leu	Ser	Leu	Pro	Glu	Gly	Gln	Ser	Leu	Arg	Leu
				260					265					270
Val	Cys	Ala	Val	Asp	Ala	Val	Asp	Ser	Asn	Pro	Pro	Ala	Arg	Leu
				275					280					285
Ser	Leu	Ser	Trp	Arg	Gly	Leu	Thr	Leu	Cys	Pro	Ser	Gln	Pro	Ser
				290					295					300
Asn	Pro	Gly	Val	Leu	Glu	Leu	Pro	Trp	Val	His	Leu	Arg	Asp	Ala
				305					310					315
Ala	Glu	Phe	Thr	Cys	Arg	Ala	Gln	Asn	Pro	Leu	Gly	Ser	Gln	Gln
				320					325					330
Val	Tyr	Leu	Asn	Val	Ser	Leu	Gln	Ser	Lys	Ala	Thr	Ser	Gly	Val
				335					340					345
Thr	Gln	Gly	Val	Val	Gly	Gly	Ala	Gly	Ala	Thr	Ala	Leu	Val	Phe
				350					355					360
Leu	Ser	Phe	Cys	Val	Ile	Phe	Val	Val	Val	Arg	Ser	Cys	Arg	Lys
				365					370					375
Lys	Ser	Ala	Arg	Pro	Ala	Ala	Gly	Val	Gly	Asp	Thr	Gly	Ile	Glu
				380					385					390
Asp	Ala	Asn	Ala	Val	Arg	Gly	Ser	Ala	Ser	Gln	Gly	Pro	Leu	Thr
				395					400					405

Glu	Pro	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala
				410					415					420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser
				425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu
				440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg		
				455					460					

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgccagtg gacctgccga ggtcggcagc acagagctct ggagatgaag 50
 accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100
 cctggaggag gaggatatca caggacacctg gtacgtgaag gccatgggtg 150
 tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200
 aaggtgacag ccctggggcg tgggaagttg gaagccacgt tcaccttcac 250
 gagggaggat cgggtgatcc agaagaaaat cctgatgcg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcccc ggagggacca ctacatcttt tactgcaaag accagcacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccca 550
 acactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctacc tccagccatg acccttcctc 650
 gctcccaccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20					25					30				
Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg
			35						40					45
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly
			50						55					60
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile
			65						70					75
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr
			80						85					90
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro
			95						100					105
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly
			110						115					120
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr
			125						130					135
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys
			140						145					150
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser
			155						160					165
Cys	Val	Pro	Glu	His										
			170											

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 164
 ggagatgaag accctgttcc tgggtg 26

<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
gtcctccgga aagtccttat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
gcctagtgtt cggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
caggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgtccttca ccctggagga ggaggatatc acaggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

1000 900 800 700 600 500 400 300 200 100 0

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cagaggtctc acagcagcca aggaacctgg gggccgctcc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 150
gtagggggag agaccaggat catcaagggg ttcgagtgc agcctcactc 200
ccagccctgg caggcagccc tggtcgagaa gacgcggcta ctctgtggg 250
cgacgtcat cgccccaga tggctcctga cagcagccca ctgcctcaag 300
ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggagg 350
ctgtgagcag acccgacag cactgagtc cttccccac cccggcttca 400
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctgggt gtgcgacccc tcacctctc 500
ctcacgctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600
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cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
gccaggggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750
attatctcct ggggccagga tccgtgtgcg atcacccgaa agcctggtgt 800
ctacacgaaa gtctgcaaat atgtggactg gatccaggag acgatgaaga 850
acaattagac tggaccacc caccacagcc catcaccctc catttccact 900
tggtgtttgg ttctgtttca ctctgttaat aagaaaccct aagccaagac 950
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tgtatcccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150
aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaa 1204

<210> 170
<211> 250
<212> PRT
<213> Homo sapiens

<400> 170
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
1 5 10 15

<400> 171
ggctgcggga ctggaagtca tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcag 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgtgtagaca ccaggctttc ggggtg 25

<210> 176
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<213> Artificial

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<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctggtc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

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<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaat atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaagg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttgtt cttggtgttg ggcaagtcatt 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca ttgcatatg gaaaggaagg ctatgcagaa 400

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
				215					220					

<210> 181
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 181
 gtgtttctgct ggagccgatg cc 22

<210> 182
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 182
 gacatggaca atgacagg 18

<210> 183
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 183
 cctttcagga tgtaggag 18

<210> 184
 <211> 18
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 185
gcatcctgat atgacttgct acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 186
tacaagaggg aagaggagtt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-52
<223> Synthetic construct.

<400> 187
gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50
cc 52

<210> 188
<211> 573
<212> DNA
<213> Homo sapiens

<400> 188
cagaaatgca gggaccattg cttcttccag gcctotgctt tctgctgagc 50
ctctttggag ctgtgactca gaaaacaaa acttctgtg ctaagtgcc 100

cccaaatgct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150
 atactttctgg atctggggcag aaactattca cattccccctt ggagacatgt 200
 aacgccaggc atggtgggctc ggcctgttaa tcccagttct ttgggaagcc 250
 aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
 atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500
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 ccaaataaag tacttatatt ctc 573

<210> 189
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 189
 Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
 1 5 10 15
 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
 20 25 30
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
 35 40 45
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
 50 55 60
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
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<210> 190
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 190
 aggaccatt gcttcttcca ggcc 24

<210> 191
 <211> 24
 <212> DNA
 <213> Artificial

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<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
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<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
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<222> 1-50
<223> Synthetic construct.

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<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
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gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200

gtgtgggcgt aactcacagc cgtggcagggt ggggctgttt gagggcacca 250

gcctgcgctg cgggggtgtc cttattgacc acagggtgggt cctcacagcg 300

gctcactgca gcggcagcag gtactgggtg cgcttggggg aacacagcct 350

cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400

cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450

ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500

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cgggagaatc acgagcaaca tgggtgtgtg aggcggcgtc ccggggcagg 700

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<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser	1	5	10	15
Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu				

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<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met	Ser	Gly	Glu	Leu	Ser	Asn	Arg	Phe	Gln	Gly	Gly	Lys	Ala	Phe	1	5	10	15
Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn	20	25	30	
Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu	35	40	45	
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp	50	55	60	
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met	65	70	75	
Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys	80	85	90	
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr	95	100	105	
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu	110	115	120	
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro	125	130	135	
Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro	140	145	150	

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

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gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200
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cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300
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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg	1	5	10	15
Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro	20	25	30	
Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val	35	40	45	
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro	50	55	60	
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg	65	70	75	
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu	80	85	90	
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe	95	100	105	
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys	110	115	120	
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu	125	130	135	
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg	140	145	150	
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp	155	160	165	

Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu	170	175	180
Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Ile Ser Arg	185	190	195
Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu	200	205	210
Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp	215	220	225
Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr	230	235	240
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp	245	250	255
Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro	260	265	270
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr	275	280	285
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu	290	295	300
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu	305	310	315
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr	320	325	330
Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp	335	340	345
Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu	350	355	360
Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe	365	370	375
Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys	380	385	390
Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu	395	400	405
Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys	410	415	420
Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala	425	430	435
Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp	440	445	450
Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser			

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Ser Pro Arg Arg	Leu Ala Asn Lys Arg	Ile Ser Gln Ile Lys Ser			
	470	475			480
Lys Lys Phe Arg	Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg Phe				
	485	490			495
Ser Ser Glu Cys	Phe Met Asp Leu Val Cys Pro Glu Lys Cys Arg				
	500	505			510
Cys Glu Gly Thr	Ile Val Asp Cys Ser Asn Gln Lys Leu Val Arg				
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Ile Pro Ser His	Leu Pro Glu Tyr Val Thr Asp Leu Arg Leu Asn				
	530	535			540
Asp Asn Glu Val	Ser Val Leu Glu Ala Thr Gly Ile Phe Lys Lys				
	545	550			555
Leu Pro Asn Leu	Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Lys				
	560	565			570
Glu Val Arg Glu	Gly Ala Phe Asp Gly Ala Ala Ser Val Gln Glu				
	575	580			585
Leu Met Leu Thr	Gly Asn Gln Leu Glu Thr Val His Gly Arg Val				
	590	595			600
Phe Arg Gly Leu	Ser Gly Leu Lys Thr Leu Met Leu Arg Ser Asn				
	605	610			615
Leu Ile Ser Cys	Val Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser				
	620	625			630
Val Arg Leu Leu	Ser Leu Tyr Asp Asn Arg Ile Thr Thr Ile Thr				
	635	640			645
Pro Gly Ala Phe	Thr Thr Leu Val Ser Leu Ser Thr Ile Asn Leu				
	650	655			660
Leu Ser Asn Pro	Phe Asn Cys Asn Cys His Leu Ala Trp Leu Gly				
	665	670			675
Lys Trp Leu Arg	Lys Arg Arg Ile Val Ser Gly Asn Pro Arg Cys				
	680	685			690
Gln Lys Pro Phe	Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala				
	695	700			705
Ile Gln Asp Phe	Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln				
	710	715			720
Leu Ser Pro Arg	Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val				
	725	730			735
Val Arg Cys Ser	Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met				
	740	745			750

Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr	755	760	765
Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile	770	775	780
Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe	785	790	795
Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg	800	805	810
Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu	815	820	825
Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu	830	835	840
Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly	845	850	855
Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu	860	865	870
Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser	875	880	885
Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr	890	895	900
His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala	905	910	915
Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr	920	925	930
Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr	935	940	945
Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile	950	955	960
Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser	965	970	975
His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly	980	985	990
Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys	995	1000	1005
Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys	1010	1015	1020
Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile	1025	1030	1035
Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys			

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
1340 1345 1350

Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
1355 1360 1365

Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
1370 1375 1380

Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
1385 1390 1395

Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
1400 1405 1410

Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
1415 1420 1425

Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
1430 1435 1440

Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
1445 1450 1455

Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
1460 1465 1470

Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
1475 1480 1485

Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
1490 1495 1500

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
1505 1510 1515

Glu Cys Gly Cys Leu Ala Cys Ser
1520

<210> 199
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 199
atggagattc ctgccaaactt gccg 24

<210> 200
<211> 24
<212> DNA
<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttggcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
ggatgcagga cgctccoctg agctgcctgt caccgactag gtggagcagt 50
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100
gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300
agagcggcta caacaccaca gccccgaagg tcctggatga cggcagcatc 350
gactatggca tcttccagat caacagcttc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtgcg ctgctcagcc ttgatcactg 450
atgacctcac agatgcaatt atctgtgccg ggaaaattgt taaagagaca 500
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550
cctgtccgag tggaaaaaag gctgtgaggt ttcctaaact ggaactggac 600
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650
cctgtgtcat cttgtcccgt ttcctcccaa tttccttctt caaacttgga 700
gagggaaaat taagctatac ttttaagaaa ataaatattt ccattttaat 750
gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr
 1 5 10 15
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
 20 25 30
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 205
ctcattggct gcctgggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgaacca aggtctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaactgg caaaaatatt ctcgagggct ggcctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
caggccattht gcatcccact gtccttgtgt tcggagccag gccacaccgt 50
octcagcagt gtcattgtgtt aaaaacgcca agctgaatat atcatgcccc 100
tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctattht actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
gaggaatata ccacaggcat ggcagactgc atcttagtca acagccagtt 350
cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400
ctgatgtcct ctatccatct ctaaattgtca ccagctttga ctcagttggt 450
cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500
ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550
ccctagtaca gctgcgtgga agattgacat cccaagattg ggagaggggt 600
catctgatcg tggcagggtg ttatgacgag agagtccctg agaatgtgga 650
acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700
atgtgacctt cttgaggtct ttctcagaca aacagaaaat ctccctcctc 750
cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800
tgtccctctg gaagccatgt acatgcagtg cccagtcatt gctgttaatt 850
cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900
gagcctgacc cgggtgcactt ctcagaagca atagaaaagt tcatccgtga 950
accttcctta aaagccacca tgggcctggc tggaagagcc agagtgaagg 1000
aaaaattttc ccctgaagca tttacagaac agctctaccg atatgttacc 1050
aaactgctgg tataatcaga ttgtttttta gatctccatt aatgtcattt 1100
ttatggattg tagaccaggt tttgaaacca aaaaagaaac ctagaatcta 1150
atgcagaaga gatcttttaa aaaataaact tgagtcttga atgtgagcca 1200
ctttcctata taccacacct cctgtccac ttttcagaaa aaccatgtct 1250
tttatgctat aatcattcca aattttgcca gtgttaagtt acaaattgtg 1300
tgtcattcca tgttcagcag agtattttaa ttatattttc tcgggattat 1350
tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400
atagtttaag tgtgtatcat tatcaaagtt gattaatttg gttcatagt 1450
ataatgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500
tcaactgtcat ctgttaggga atttttgttt gtccctgtct tgccctggatc 1550
catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600
actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaaa 1648

<210> 210

<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	
1				5					10					15	
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	
				20					25					30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	
				35					40					45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	
				50					55					60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	
				65					70					75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	
				80					85					90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	
				95					100					105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	
				110					115					120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	
				125					130					135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	
				140					145					150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	
				155					160					165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	
				170					175					180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	
				185					190					195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	
				200					205					210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	
				215					220					225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	
				230					235					240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	
				245					250					255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	
				260					265					270	

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg
275 280 285

Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
290 295 300

Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
305 310 315

Arg Tyr Val Thr Lys Leu Leu Val
320

<210> 211
<211> 1554
<212> DNA
<213> Homo sapiens

<400> 211
gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50
cttcgcgata ttcgccgtta ccttcttgct ggcgttggtg ggagccgtgc 100
tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200
tttgcatgag ttcctgggta atttgcata gagatatggg cctgtggtct 250
ccttctgggt tggcaggcgc ctcgtgggta gtttgggcac tgttgatgta 300
ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350
gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaaa 400
accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500
gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
gttttgctat gaagtctggt acacagatgg taatgggtag tacatttgaa 600
gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650
tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800
tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850
gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

				140						145					150
Asp	Lys	Trp	Leu	Ser 155	Tyr	Pro	Glu	Thr	Gln	His	Val	Pro	Leu	Ser	165
Gln	His	Met	Leu	Gly 170	Phe	Ala	Met	Lys	Ser	Val	Thr	Gln	Met	Val	180
Met	Gly	Ser	Thr	Phe 185	Glu	Asp	Asp	Gln	Glu	Val	Ile	Arg	Phe	Gln	195
Lys	Asn	His	Gly	Thr 200	Val	Trp	Ser	Glu	Ile	Gly	Lys	Gly	Phe	Leu	210
Asp	Gly	Ser	Leu	Asp 215	Lys	Asn	Met	Thr	Arg	Lys	Lys	Gln	Tyr	Glu	225
Asp	Ala	Leu	Met	Gln 230	Leu	Glu	Ser	Val	Leu	Arg	Asn	Ile	Ile	Lys	240
Glu	Arg	Lys	Gly	Arg 245	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	Asp	Ser	255
Leu	Val	Gln	Gly	Asn 260	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	Ser	270
Met	Ile	Phe	Ser	Leu 275	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys	285
Thr	Trp	Ala	Ile	Cys 290	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys	300
Lys	Leu	Tyr	Glu	Glu 305	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	315
Thr	Pro	Glu	Lys	Ile 320	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	330
Cys	Glu	Thr	Val	Arg 335	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	345
Leu	Gln	Asp	Ile	Glu 350	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	360
Glu	Thr	Leu	Val	Leu 365	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	375
Asn	Thr	Trp	Pro	Ser 380	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp	390
Asp	Glu	Leu	Val	Met 395	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly	405
Thr	Gln	Glu	Cys	Pro 410	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr	420
Val	Leu	Leu	Ser	Val 425	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val	435

Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	Leu	Val	Thr	Ser	Ser
				440					445					450

Arg	Glu	Glu	Ala	Trp	Ile	Thr	Val	Ser	Lys	Arg	Tyr
				455					460		

<210> 213
 <211> 759
 <212> DNA
 <213> Homo sapiens

<400> 213
 ctagatttgt cggcttgccg ggagacttca ggagtcgctg tctctgaact 50
 tccagcctca gagaccgccg cccttgtccc cgagggccat gggccgggtc 100
 tcagggttg tgccctctcg ctctctgacg ctcttgccgc atctggtggt 150
 cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
 ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250
 gccgcgctct ctgtcaccct gggcctcttt gcagtggagc tggccgggtt 300
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
 gggctcactg tagtgcaccc gtggccctgt ccttcttcat attcgagcgt 400
 tgggagtgca ctacgtattg gtacattttt gtctttctgca gtgcccttcc 450
 agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600
 ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
 tgttttgtag taacattaag acttatatac agttttaggg gacaattaa 750
 aaaaaaaaa 759

<210> 214
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 214
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
 1 5 10 15
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
 20 25 30
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
 35 40 45

Tyr	Asp	Lys	Gln	Asp	Ile	Gln	Leu	Val	Ala	Ala	Leu	Ser	Val	Thr	
				50					55					60	
Leu	Gly	Leu	Phe	Ala	Val	Glu	Leu	Ala	Gly	Phe	Leu	Ser	Gly	Val	
				65					70					75	
Ser	Met	Phe	Asn	Ser	Thr	Gln	Ser	Leu	Ile	Ser	Ile	Gly	Ala	His	
				80					85					90	
Cys	Ser	Ala	Ser	Val	Ala	Leu	Ser	Phe	Phe	Ile	Phe	Glu	Arg	Trp	
				95					100					105	
Glu	Cys	Thr	Thr	Tyr	Trp	Tyr	Ile	Phe	Val	Phe	Cys	Ser	Ala	Leu	
				110					115					120	
Pro	Ala	Val	Thr	Glu	Met	Ala	Leu	Phe	Val	Thr	Val	Phe	Gly	Leu	
				125					130					135	
Lys	Lys	Lys	Pro	Phe											
				140											

<210> 215
 <211> 697
 <212> DNA
 <213> Homo sapiens

<400> 215
 tcccggaccc tgccgccttg ccactatgtc ccgccgctct atgctgcttg 50
 cctgggctct cccagcctc ctgcgactcg gagcggctca ggagacagaa 100
 gaccgggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150
 ggcacagag tgcgccagc acctgagcct gcccttacgc tatgtggtgg 200
 tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
 caggcccga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
 cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
 gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
 tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
 ccaggccatc cgggcagccc aggtctact ggctgoggt gtggctcagg 500
 gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
 aactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
 ctaccgctcc cctgaggcc ctgctgatcc gcacccatt cctcccctcc 650
 catggccaaa aaccccaactg tctccttctc caataaagat gtagctc 697

<210> 216
 <211> 196
 <212> PRT

<213> Homo sapiens

<400> 216

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu
1 5 10 15
Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
20 25 30
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
35 40 45
Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
50 55 60
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
65 70 75
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
80 85 90
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
95 100 105
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
110 115 120
Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
125 130 135
Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
140 145 150
Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
155 160 165
Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
170 175 180
Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
185 190 195
Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

Met Gln Leu Thr Arg Cys Cys Phe Val Phe Leu Val Gln Gly Ser
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Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser
20 25 30

Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg
35 40 45

Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met
50 55 60

Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala
65 70 75

Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro
80 85 90

Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe
95 100 105

Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly
110 115 120

Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln
125 130 135

His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro
140 145 150

Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile
155 160 165

Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu
170 175 180

Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro
185 190 195

Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp
200 205 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
				65					70					75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
				80					85					90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
				95					100					105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
				110					115					120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
				125					130					135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
				140					145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
				155					160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
				185					190					195	
Phe	Leu	Val	Phe	Pro	Leu										
				200											

<210> 221
 <211> 20
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

 <400> 221
 acggctcacc atgggctccg 20

 <210> 222
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 222
 aggaagagga gcccttggag tccg 24

 <210> 223
 <211> 40

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
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<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
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tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250
tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300
gtgaaggttt gaagagtata aaccaggtg agacagcacc ctctatgcga 350
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gtcattatct tgctgcatgt attctggggc attgtatttt ttgatggctg 550
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<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly	
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Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu	
				20					25					30	
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	
				35					40					45	
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	
				50					55					60	
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	
				65					70					75	
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	
				80					85					90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	
				95					100					105	
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	
				110					115					120	
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	
				125					130					135	
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	
				140					145					150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	
				155					160					165	
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	
				170					175					180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	
				185					190					195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	
				200					205					210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	
				215					220					225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	
				230					235					240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	
				245					250					255	

Ser Arg

<210> 226

<211> 3939
 <212> DNA
 <213> Homo sapiens

<400> 226
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 agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200
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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

Met	Phe	Ala	Leu	Gly	Leu	Pro	Phe	Leu	Val	Leu	Leu	Val	Ala	Ser
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Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20					25					30

	320		325		330
Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala	335		340		345
Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly	350		355		360
Ser Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser	365		370		375
Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe	380		385		390
Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val	395		400		405
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys	410		415		420
Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala	425		430		435
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe	440		445		450
Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val	455		460		465
Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn	470		475		480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly	485		490		495
Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile	500		505		510
Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile	515		520		525
Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu	530		535		540
Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr	545		550		555
Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys	560		565		570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met	575		580		585
Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro	590		595		600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile	605		610		615

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 cctccctgag gatgtggagc ccgggactct ggtggccatg ctaacagcca 1550
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 aggggagaca cagaagggac ttttggcctg gattgggagc cagactctgg 1650

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				35					40					45
Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp
				50					55					60
Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser
				65					70					75
Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala
				80					85					90
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val
				95					100					105
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn
				110					115					120
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu
				125					130					135
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala
				140					145					150
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe
				155					160					165
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe
				170					175					180
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly
				185					190					195
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu
				200					205					210
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala
				215					220					225
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser
				230					235					240
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro
				245					250					255
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr
				260					265					270
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu
				275					280					285
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala
				290					295					300
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp
				305					310					315

Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn
				320					325					330
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile
				335					340					345
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala
				350					355					360
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr
				365					370					375
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala
				380					385					390
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu
				395					400					405
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met
				410					415					420
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val
				425					430					435
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile
				440					445					450
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro
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Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu
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Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr
				485					490					495
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val
				500					505					510
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser
				515					520					525
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly
				530					535					540
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val
				545					550					555
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu
				560					565					570
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr
				575					580					585
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu
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 <222> full
 <223> Synthetic oligonucleotide probe

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<210> 232
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 232
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<210> 233
 <211> 2786
 <212> DNA
 <213> Homo sapiens

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 acttgaagct caattttctg aaatctccct cctccttcaa tcggcctgtg 200
 gatgtcctgg tcccatctgt cagtctgcag gcatttaa at ccttcctgag 250
 atcccagggc ttagagtacg cagtgacaat tgaggacctg caggcccttt 300
 tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
 agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400
 cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450
 agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
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 <211> 421
 <212> PRT
 <213> Homo sapiens

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 Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
 35 40 45
 Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe
 50 55 60
 Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala
 65 70 75
 Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr
 80 85 90
 Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met
 95 100 105
 Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr
 110 115 120
 Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn
 125 130 135
 Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly
 140 145 150
 His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr
 155 160 165

Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	170	175	180
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	185	190	195
Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	200	205	210
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	215	220	225
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	230	235	240
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	245	250	255
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	260	265	270
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	275	280	285
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	290	295	300
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	305	310	315
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	320	325	330
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	335	340	345
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	350	355	360
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	365	370	375
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	380	385	390
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	395	400	405
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	410	415	420

Tyr

- <210> 235
- <211> 1743
- <212> DNA
- <213> Homo sapiens

<400> 235

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 attcaataaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236

<211> 417

<212> PRT

<213> Homo sapiens

<400> 236

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Pro	Arg	Pro	Ser	Ser	Thr	Lys	Ser	Thr	Pro	Ala	Ser	Gln	Val	Tyr	35	40	45	
Ser	Leu	Asn	Thr	Asp	Phe	Ala	Phe	Arg	Leu	Tyr	Arg	Arg	Leu	Val	50	55	60	
Leu	Glu	Thr	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Val	65	70	75	
Ser	Thr	Ser	Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	His	Ser	Val	Thr	80	85	90	
Lys	Thr	Gln	Ile	Leu	Gln	Gly	Leu	Gly	Phe	Asn	Leu	Thr	His	Thr	95	100	105	
Pro	Glu	Ser	Ala	Ile	His	Gln	Gly	Phe	Gln	His	Leu	Val	His	Ser	110	115	120	
Leu	Thr	Val	Pro	Ser	Lys	Asp	Leu	Thr	Leu	Lys	Met	Gly	Ser	Ala	125	130	135	
Leu	Phe	Val	Lys	Lys	Glu	Leu	Gln	Leu	Gln	Ala	Asn	Phe	Leu	Gly	140	145	150	
Asn	Val	Lys	Arg	Leu	Tyr	Glu	Ala	Glu	Val	Phe	Ser	Thr	Asp	Phe	155	160	165	
Ser	Asn	Pro	Ser	Ile	Ala	Gln	Ala	Arg	Ile	Asn	Ser	His	Val	Lys	170	175	180	
Lys	Lys	Thr	Gln	Gly	Lys	Val	Val	Asp	Ile	Ile	Gln	Gly	Leu	Asp	185	190	195	
Leu	Leu	Thr	Ala	Met	Val	Leu	Val	Asn	His	Ile	Phe	Phe	Lys	Ala				

				200					205					210
Lys	Trp	Glu	Lys	Pro 215	Phe	His	Leu	Glu	Tyr 220	Thr	Arg	Lys	Asn	Phe 225
Pro	Phe	Leu	Val	Gly 230	Glu	Gln	Val	Thr	Val 235	Gln	Val	Pro	Met	Met 240
His	Gln	Lys	Glu	Gln 245	Phe	Ala	Phe	Gly	Val 250	Asp	Thr	Glu	Leu	Asn 255
Cys	Phe	Val	Leu	Gln 260	Met	Asp	Tyr	Lys	Gly 265	Asp	Ala	Val	Ala	Phe 270
Phe	Val	Leu	Pro	Ser 275	Lys	Gly	Lys	Met	Arg 280	Gln	Leu	Glu	Gln	Ala 285
Leu	Ser	Ala	Arg	Thr 290	Leu	Ile	Lys	Trp	Ser 295	His	Ser	Leu	Gln	Lys 300
Arg	Trp	Ile	Glu	Val 305	Phe	Ile	Pro	Arg	Phe 310	Ser	Ile	Ser	Ala	Ser 315
Tyr	Asn	Leu	Glu	Thr 320	Ile	Leu	Pro	Lys	Met 325	Gly	Ile	Gln	Asn	Ala 330
Phe	Asp	Lys	Asn	Ala 335	Asp	Phe	Ser	Gly	Ile 340	Ala	Lys	Arg	Asp	Ser 345
Leu	Gln	Val	Ser	Lys 350	Ala	Thr	His	Lys	Ala 355	Val	Leu	Asp	Val	Ser 360
Glu	Glu	Gly	Thr	Glu 365	Ala	Thr	Ala	Ala	Thr 370	Thr	Thr	Lys	Phe	Ile 375
Val	Arg	Ser	Lys	Asp 380	Gly	Pro	Ser	Tyr	Phe 385	Thr	Val	Ser	Phe	Asn 390
Arg	Thr	Phe	Leu	Met 395	Met	Ile	Thr	Asn	Lys 400	Ala	Thr	Asp	Gly	Ile 405
Leu	Phe	Leu	Gly	Lys 410	Val	Glu	Asn	Pro	Thr 415	Lys	Ser			

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<212> DNA

<220>

<222> 1-23

<400> 237

<210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
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<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
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<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
ggtataggcg gaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
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<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc 50

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Thr	Asn	Ser	Glu	Phe 95	Ser	Thr	Ala	Ser	Ser 100	Gly	Ile	Ser	Ile	Ala 105
Thr	Asn	Ser	Glu	Ser 110	Ser	Thr	Thr	Ser	Ser 115	Gly	Ala	Ser	Thr	Ala 120
Thr	Asn	Ser	Glu	Ser 125	Ser	Thr	Pro	Ser	Ser 130	Gly	Ala	Ser	Thr	Val 135
Thr	Asn	Ser	Gly	Ser 140	Ser	Val	Thr	Ser	Ser 145	Gly	Ala	Ser	Thr	Ala 150
Thr	Asn	Ser	Glu	Ser 155	Ser	Thr	Val	Ser	Ser 160	Arg	Ala	Ser	Thr	Ala 165
Thr	Asn	Ser	Glu	Ser 170	Ser	Thr	Leu	Ser	Ser 175	Gly	Ala	Ser	Thr	Ala 180
Thr	Asn	Ser	Asp	Ser 185	Ser	Thr	Thr	Ser	Ser 190	Gly	Ala	Ser	Thr	Ala 195
Thr	Asn	Ser	Glu	Ser 200	Ser	Thr	Thr	Ser	Ser 205	Gly	Ala	Ser	Thr	Ala 210
Thr	Asn	Ser	Glu	Ser 215	Ser	Thr	Val	Ser	Ser 220	Arg	Ala	Ser	Thr	Ala 225
Thr	Asn	Ser	Glu	Ser 230	Ser	Thr	Thr	Ser	Ser 235	Gly	Ala	Ser	Thr	Ala 240
Thr	Asn	Ser	Glu	Ser 245	Arg	Thr	Thr	Ser	Asn 250	Gly	Ala	Gly	Thr	Ala 255
Thr	Asn	Ser	Glu	Ser 260	Ser	Thr	Thr	Ser	Ser 265	Gly	Ala	Ser	Thr	Ala 270
Thr	Asn	Ser	Asp	Ser 275	Ser	Thr	Val	Ser	Ser 280	Gly	Ala	Ser	Thr	Ala 285
Thr	Asn	Ser	Glu	Ser 290	Ser	Thr	Thr	Ser	Ser 295	Gly	Ala	Ser	Thr	Ala 300
Thr	Asn	Ser	Glu	Ser 305	Ser	Thr	Thr	Ser	Ser 310	Gly	Ala	Ser	Thr	Ala 315
Thr	Asn	Ser	Asp	Ser 320	Ser	Thr	Thr	Ser	Ser 325	Gly	Ala	Gly	Thr	Ala 330
Thr	Asn	Ser	Glu	Ser 335	Ser	Thr	Val	Ser	Ser 340	Gly	Ile	Ser	Thr	Val 345
Thr	Asn	Ser	Glu	Ser 350	Ser	Thr	Pro	Ser	Ser 355	Gly	Ala	Asn	Thr	Ala 360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala

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<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

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Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly
215 220 225

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230 235 240

Ser Val Ala Asn Ile Met Pro
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<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

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<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctct gcttcctttc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

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<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu
 50 55 60
 Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
 65 70 75
 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

Glu	Val	Asn	Arg	Glu 380	Thr	Gln	Gln	Trp	Tyr 385	Thr	Val	Thr	His	Pro 390
Val	Pro	Thr	Pro	Arg 395	Pro	Gly	Ala	Cys	Ile 400	Thr	Asn	Ser	Ala	Arg 405
Glu	Arg	Lys	Ile	Asn 410	Ser	Ser	Leu	Gln	Leu 415	Pro	Asp	Arg	Val	Leu 420
Asn	Phe	Leu	Lys	Asp 425	His	Phe	Leu	Met	Asp 430	Gly	Gln	Val	Arg	Ser 435
Arg	Met	Leu	Leu	Leu 440	Gln	Pro	Gln	Ala	Arg 445	Tyr	Gln	Arg	Val	Ala 450
Val	His	Arg	Val	Pro 455	Gly	Leu	His	His	Thr 460	Tyr	Asp	Val	Leu	Phe 465
Leu	Gly	Thr	Gly	Asp 470	Gly	Arg	Leu	His	Lys 475	Ala	Val	Ser	Val	Gly 480
Pro	Arg	Val	His	Ile 485	Ile	Glu	Glu	Leu	Gln 490	Ile	Phe	Ser	Ser	Gly 495
Gln	Pro	Val	Gln	Asn 500	Leu	Leu	Leu	Asp	Thr 505	His	Arg	Gly	Leu	Leu 510
Tyr	Ala	Ala	Ser	His 515	Ser	Gly	Val	Val	Gln 520	Val	Pro	Met	Ala	Asn 525
Cys	Ser	Leu	Tyr	Arg 530	Ser	Cys	Gly	Asp	Cys 535	Leu	Leu	Ala	Arg	Asp 540
Pro	Tyr	Cys	Ala	Trp 545	Ser	Gly	Ser	Ser	Cys 550	Lys	His	Val	Ser	Leu 555
Tyr	Gln	Pro	Gln	Leu 560	Ala	Thr	Arg	Pro	Trp 565	Ile	Gln	Asp	Ile	Glu 570
Gly	Ala	Ser	Ala	Lys 575	Asp	Leu	Cys	Ser	Ala 580	Ser	Ser	Val	Val	Ser 585
Pro	Ser	Phe	Val	Pro 590	Thr	Gly	Glu	Lys	Pro 595	Cys	Glu	Gln	Val	Gln 600
Phe	Gln	Pro	Asn	Thr 605	Val	Asn	Thr	Leu	Ala 610	Cys	Pro	Leu	Leu	Ser 615
Asn	Leu	Ala	Thr	Arg 620	Leu	Trp	Leu	Arg	Asn 625	Gly	Ala	Pro	Val	Asn 630
Ala	Ser	Ala	Ser	Cys 635	His	Val	Leu	Pro	Thr 640	Gly	Asp	Leu	Leu	Leu 645
Val	Gly	Thr	Gln	Gln 650	Leu	Gly	Glu	Phe	Gln 655	Cys	Trp	Ser	Leu	Glu 660
Glu	Gly	Phe	Gln	Gln	Leu	Val	Ala	Ser	Tyr	Cys	Pro	Glu	Val	Val

665										670					675				
Glu	Asp	Gly	Val	Ala	Asp	Gln	Thr	Asp		Glu	Gly	Gly	Ser	Val	Pro				
				680						685					690				
Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser		Ala	Pro	Ala	Gly	Gly	Lys				
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Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr		Trp	Lys	Glu	Phe	Leu	Val				
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Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val		Leu	Leu	Pro	Val	Leu	Phe				
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Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met		Lys	Val	Phe	Leu	Lys	Gln				
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Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys		Thr	Cys	Pro	Val	Val	Leu				
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Pro	Pro	Glu	Thr	Arg	Pro	Leu	Asn	Gly		Leu	Gly	Pro	Pro	Ser	Thr				
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Pro	Leu	Asp	His	Arg	Gly	Tyr	Gln	Ser		Leu	Ser	Asp	Ser	Pro	Pro				
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Gly	Ala	Arg	Val	Phe	Thr	Glu	Ser	Glu		Lys	Arg	Pro	Leu	Ser	Ile				
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Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro		Val	Cys	Pro	Arg	Pro	Arg				
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Val	Arg	Leu	Gly	Ser	Glu	Ile	Arg	Asp		Ser	Val	Val							
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<212> DNA
<213> Artificial
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<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

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<210>	255
<211>	24
<212>	DNA
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<223> Synthetic construct.
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<400> 255
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<210> 256
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<212> DNA
<213> Artificial

<220>
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<223> Synthetic construct.

<400> 256
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<210> 257
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<212> DNA
<213> Artificial

<220>
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<222> 1-41
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<210> 258
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<223> unknown base

<400> 259
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attcctgttt tagctgaaga attgtattac atttgagag taaaaaactt 4550

aaacacgaaa aaa 4563

<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg
20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
230 235 240

				50					55					60	
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys	
				65					70					75	
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu	
				80					85					90	
Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly	
				95					100					105	
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro	
				110					115					120	
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala	
				125					130					135	
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu	
				140					145					150	
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val	
				155					160					165	
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro	
				170					175					180	
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu	
				185					190					195	
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys	
				200					205					210	
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp	
				215					220					225	
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala	
				230					235					240	
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu	
				245					250					255	
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala	
				260					265					270	
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro	
				275					280					285	
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile	
				290					295					300	
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp	
				305					310					315	
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val	
				320					325					330	
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala	
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Leu Leu Lys Val Tyr
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<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val	320	325	330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val	335	340	345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp	350	355	360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn	365	370	375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr	380	385	390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr	395	400	405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe	410	415	420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys	425	430	435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr	440	445	450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp	455	460	465

Gly

<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 268
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 gtcattctca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
 tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
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 agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
 agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450
 tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500

atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000
 caaaccttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050
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 cca 2103

<210> 269

<211> 423

<212> PRT

<213> Homo sapiens

<400> 269

Met	Met	Tyr	Arg	Pro	Asp	Val	Val	Arg	Ala	Arg	Lys	Arg	Val	Cys	1	5	10	15
Trp	Glu	Pro	Trp	Val	Ile	Gly	Leu	Val	Ile	Phe	Ile	Ser	Leu	Ile	20	25	30	
Val	Leu	Ala	Val	Cys	Ile	Gly	Leu	Thr	Val	His	Tyr	Val	Arg	Tyr	35	40	45	
Asn	Gln	Lys	Lys	Thr	Tyr	Asn	Tyr	Tyr	Ser	Thr	Leu	Ser	Phe	Thr	50	55	60	
Thr	Asp	Lys	Leu	Tyr	Ala	Glu	Phe	Gly	Arg	Glu	Ala	Ser	Asn	Asn	65	70	75	
Phe	Thr	Glu	Met	Ser	Gln	Arg	Leu	Glu	Ser	Met	Val	Lys	Asn	Ala	80	85	90	
Phe	Tyr	Lys	Ser	Pro	Leu	Arg	Glu	Glu	Phe	Val	Lys	Ser	Gln	Val	95	100	105	
Ile	Lys	Phe	Ser	Gln	Gln	Lys	His	Gly	Val	Leu	Ala	His	Met	Leu	110	115	120	
Leu	Ile	Cys	Arg	Phe	His	Ser	Thr	Glu	Asp	Pro	Glu	Thr	Val	Asp	125	130	135	
Lys	Ile	Val	Gln	Leu	Val	Leu	His	Glu	Lys	Leu	Gln	Asp	Ala	Val	140	145	150	
Gly	Pro	Pro	Lys	Val	Asp	Pro	His	Ser	Val	Lys	Ile	Lys	Lys	Ile	155	160	165	
Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys	Cys	Gly	Thr	170	175	180	
Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	Gly	Gly	185	190	195	
Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	200	205	210	
Trp	Asp	Gly	Ser	His	Arg	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr	215	220	225	

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	230	235	240
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	245	250	255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	260	265	270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	275	280	285
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	290	295	300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	305	310	315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	320	325	330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	335	340	345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	350	355	360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	365	370	375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly	380	385	390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly	395	400	405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys	410	415	420

Thr Gly Ile

<210> 270
 <211> 1170
 <212> DNA
 <213> Homo sapiens

<400> 270
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<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

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 20 25 30

Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu
 35 40 45

Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe
 50 55 60

Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
 65 70 75

Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
 80 85 90

Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys
 95 100 105

Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met
 110 115 120

Val Pro Val Gln Trp Ser Asp Met Val Thr Leu Lys Ala Arg Met
 125 130 135

Thr Asn Tyr Gly Leu Pro Arg Tyr Arg Trp Leu Thr His Ala Trp
 140 145 150

Asn Phe Phe Gln Arg Glu Phe Lys Cys Cys Gly Val Val Tyr Phe
 155 160 165

Thr Asp Trp Leu Glu Met Thr Glu Met Asp Trp Pro Pro Asp Ser

170	175	180
Cys Cys Val Arg Glu Phe Pro Gly Cys Ser Lys Gln Ala His Gln		
185	190	195
Glu Asp Leu Ser Asp Leu Tyr Gln Glu Gly Cys Gly Lys Lys Met		
200	205	210
Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe		
215	220	225
Leu Gly Ile Ser Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu		
230	235	240
Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro		
245	250	255
Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His		
260	265	270
Leu Ser Cys Pro Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg		
275	280	285
Ile Phe Glu His Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe		
290	295	300
Glu Met Glu Glu Leu		
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<210> 274
 <211> 2063
 <212> DNA
 <213> Homo sapiens

<400> 274
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 aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga 1850
 tcaactgtgg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg 1900
 tcttcacca tccccaagcc tactagagca agaaaccagt tgtaatatata 1950
 aatgcactgc cctactgttg gtatgactac cgttacctac tgttgtcatt 2000
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[illegible]

<211> 432

<213> Homo sapiens

Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp
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Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg
20 25 30

Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser
35 40 45

Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
50 55 60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
65 70 75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
80 85 90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
110 115 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
125 130 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu
140 145 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn
155 160 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu
185 190 195

Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser
200 205 210

Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys
215 220 225

Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His
230 235 240

Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala
245 250 255

Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys	
				260					265					270	
Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp	Asn	Asp	
				275					280					285	
Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr	
				290					295					300	
Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro	
				305					310					315	
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn	
				320					325					330	
Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val	
				335					340					345	
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu	
				350					355					360	
Val	Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val	
				365					370					375	
Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser	
				380					385					390	
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys	
				395					400					405	
Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr	
				410					415					420	
Leu	Asn	Trp	Ile	Tyr	Asn	Val	Trp	Lys	Ala	Glu	Leu				
				425					430						

<210> 276
 <211> 3143
 <212> DNA
 <213> Homo sapiens

<400> 276
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 gagcatggcc ctcccagccc tgggcctgga cccctggagc ctccctgggcc 150
 ttttcctctt ccaactgctt cagctgctgc tgccgacgac gaccgcgggg 200
 ggaggcgggc agggggcccat gccaggggtc agatactatg caggggatga 250
 acgtagggca cttagcttct tccaccagaa gggcctccag gattttgaca 300
 ctctgctcct gagtgggtgat ggaaatactc tctacgtggg ggctcgagaa 350
 gccattctgg ccttgatata ccaggatcca ggggtcccca ggctaaagaa 400

catgataccg tggccagcca gtgacagaaa aaagagtga tgtgccttta 450
agaagaagag caatgagaca cagtgtttca acttcatccg tgtcctgggt 500
tcttacaatg tcacccatct ctacacctgc ggcaccttcg ccttcagccc 550
tgcttgtacc ttcatagaac ttcaagattc ctacctgttg cccatctcgg 600
aggacaaggt catggaggga aaaggccaaa gccctttga ccccgctcac 650
aagcataccg ctgtcttggg ggatgggatg ctctattctg gtactatgaa 700
caacttcctg ggcagtgagc ccatcctgat gcgcacactg ggatcccagc 750
ctgtcctcaa gaccgacaac ttctccgct ggctgcatca tgacgcctcc 800
tttgtggcag ccatcccttc gaccaggtc gtctacttct tcttcgagga 850
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cagctcccca catctacgca gtcttcacct cccagtggca ggttggcggg 1100
accaggagct ctgcggtttg tgccttctct ctcttggaca ttgaacgtgt 1150
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ccctcctctg ataaggccct gaccttcatt aaggaccatt tcctgatgga 1300
tgagcaagtg gtggggacgc ccctgctggg gaaatctggc gtggagtata 1350
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 agaagcctct tccactgtct acaatggctc cctcttgctg atagtgcagg 1950
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 caggggtaat ctgagccttc ttactcctt taccctagct gacctttca 3050
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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

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Leu	Phe	Leu	Phe	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Pro	Thr	Thr	Thr
				20					25					30
Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr
				35					40					45
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly
				50					55					60
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr
				65					70					75
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln
				80					85					90
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala
				95					100					105
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn
				110					115					120
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn
				125					130					135
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala
				140					145					150
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser
				155					160					165
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro
				170					175					180
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser
				185					190					195
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg
				200					205					210
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg
				215					220					225
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr
				230					235					240
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp
				245					250					255
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys
				260					265					270
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr
				275					280					285
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro

Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu
				590					595					600
Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln
				605					610					615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly
				620					625					630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln
				635					640					645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His
				650					655					660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala
				665					670					675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu
				680					685					690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser
				695					700					705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu
				710					715					720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His
				725					730					735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp
				740					745					750
Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala				
				755					760					

<210> 278
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 278
 ctgctggtga aatctggcgt ggag 24

<210> 279
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 279
gtctggtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
catcttgtca tgtacctggg aaccaccaca gggctgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
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cttccgtaga agtgagcatg gctgggcagc gaggcttct tctagtgggc 100
ttccttctcc ctggggtcct gctctcagag gctgccaaaa tcctgacaat 150
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
ttcttcaaga tcacggcat aatgtcacca tgcttaacca caaaagaggt 250
ccttttatgc cagattttaa aaaggaagaa aaatcatatc aagttatcag 300
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450
ggatatcatg gattccttaa agaatgagaa cttcgacatg gtgatagttg 500
aaacttttga ctactgtcct ttctgattg ctgagaagct tgggaagcca 550
tttgtggcca ttctttccac ttcatcggc tctttggaat ttgggctacc 600
aatccccttg tcttatgttc cagtattccg ttcccttgctg actgatcaca 650
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aggaggcaac agcatatgca gtctacattt gacaacacca tcaaggaaca 750
tttcacagaa ggctctaggc cagttttgtc tcatcttcta ctgaaagcag 800
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cttcccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900

agtaccacaa gacttggaga acttcattgc caagtttggg gactctggtt 950
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 ggaagacaag agatacaagt ccgcggcagt ggctgccagt gtcatoctgc 1400
 gctccacccc gctcagcccc acacagcggc tgggtgggctg gattgaccac 1450
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 aaaatccacc ttccttctca tgcgcctctc cgaatcacac cctgactctt 2000
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 gtccctgtct ctgggtgcca cagtgaagctc cttcttggct gagcaggcat 2250
 ggagactgta ggtttccaga tttctgaaa aataaaagtt tacagcgta 2300
 tctctcccca acctactaa 2320

<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282

Met	Ala	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro
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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly

260	265	270
Leu Met Glu Lys	Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn
275	280	285
Phe Ile Ala Lys	Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu
290	295	300
Gly Ser Met Val	Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu
305	310	315
Met Asn Asn Ala	Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys
320	325	330
Cys Gln Cys Ser	His Trp Pro Lys Asp	Val His Leu Ala Ala Asn
335	340	345
Val Lys Ile Val	Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His
350	355	360
Pro Ser Ile Arg	Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile
365	370	375
Met Glu Ala Ile	Gln His Gly Val Pro	Met Val Gly Ile Pro Leu
380	385	390
Phe Gly Asp Gln	Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys
395	400	405
Phe Gly Val Ser	Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu
410	415	420
Ala Leu Lys Met	Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser
425	430	435
Ala Ala Val Ala	Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser
440	445	450
Pro Thr Gln Arg	Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr
455	460	465
Gly Gly Ala Thr	His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp
470	475	480
His Glu Gln Tyr	Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu
485	490	495
Thr Leu Gly Thr	Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala
500	505	510
Val Trp Trp Leu	Arg Gly Ala Arg Lys	Val Lys Glu Thr
515	520	

<210> 283
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 283
 tgcctttgct cacctacccc aagg 24

<210> 284
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 284
 tcaggctggt ctccaaagag aggg 24

<210> 285
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 285
 cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 286
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 ccagggagag gagcggaac agaagagggg cagaagaccg gggcacttgt 450

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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
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Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser
185 190 195

Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu
200 205

<210> 288

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 288

aggcagccac cagctctgtg ctac 24

<210> 289

<211> 27

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-27

<223> Synthetic construct.

<400> 289

cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-42

<223> Synthetic construct.

<400> 290

ctgtgctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 291

gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50

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ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttcccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200
 ccgcctactc cggggctctg cgcgggcagc gtcaggccga ggctgaccgg 250
 agccagcgct ctacaggagg acctgcgctg tcgcgcgagg ggtctgggag 300
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 gaaattataa caattttgct aaacaaaaa aaaaaaaaa aaaaaaaaa 1500
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 aaaaaaaaa aaaaaaaaa 1570

<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu
1				5					10					15
Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro
			20						25					30
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
			35						40					45
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn
			50						55					60
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
			65						70					75
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
			80						85					90
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
			95						100					105
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly
			110						115					120
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
			125						130					135
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
			140						145					150
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
			155						160					165
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
			170						175					180
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
			185						190					195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
			200						205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
			215						220					225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
			230						235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
			245						250					255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe	Gly Glu Asn Glu Val Tyr	
275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser	Trp Gly Arg Trp Val Gln	
290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe	Ala Pro Cys Ile Phe His	
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr	Trp Gly Leu Val Pro Tyr	
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly	Glu Pro Ile Thr Ile Pro	
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp	Ile Asp Leu Tyr His Thr	
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu	Phe Asp Lys His Lys Thr	
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val	Leu Glu Val Asn	
380	385	

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 293
 gctgacctgg ttcccatcta ctcc 24

 <210> 294
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 294
 cccacagaca cccatgacac ttcc 24

 <210> 295
 <211> 50
 <212> DNA
 <213> Artificial

 <220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
gggcggcggg atgggggccc ggggcggcgg gcgcgcact cgctgaggcc 50
ccgacgcagg gccgggcccg gcccagggcc gaggagcgcg gcggccagag 100
cggggccgcg gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200
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 ccagggagac tgaagtggga ggatcgcttg ggcattgagaa gtcgaggctg 3000
 cagtgagtcg aggttgtgcg actgcattcc agcctggaca acagagtgag 3050
 accctgtctc 3060

<210> 297
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 297
 Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu
 1 5 10 15
 Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe
 20 25 30
 Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu
 35 40 45
 Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln
 50 55 60
 Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu
 65 70 75
 Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala
 80 85 90
 Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly
 95 100 105
 Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val
 110 115 120
 Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr
 125 130 135
 Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu
 140 145 150
 Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr
 155 160 165

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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tgcttttagca ctggggcact tcttgcttat ttctttggta ggaaaggggc 150

tcagtttgtc ttgtgggggt ggtggcaggc aggccggctt acgcctgata 200

cggccttggg ttagaaggga agggaagata aacttttata caaatgggga 250

tagctgggggt ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300

ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350

ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400

gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450

tgctgttcct gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500

tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550

atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600

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gttgtagtggg ttgtgtctgt tcccagaat gccagctct gagctgcgtg 750

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```

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<210> 302
<211> 143
<212> PRT
<213> Homo sapiens

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<400> 302
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His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe
          20          25          30

Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly
          35          40          45

Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val
          50          55          60

Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp
          65          70          75

Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr
          80          85          90

Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln
          95          100          105

Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu
          110          115          120

Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr
          125          130          135

Cys Gly Val Leu Leu Ser Phe Leu

```

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303
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 tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgttt 200
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
 50 55 60
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
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 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
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 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
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 Arg Arg Arg Asp

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 <212> DNA
 <213> Homo sapiens

<400> 305

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 <211> 262
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 <213> Homo sapiens

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 Leu Leu Pro Pro Glu Asp Ser Arg Leu Trp Gln Tyr Leu Leu Ser
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Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu
65 70 75

Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln
80 85 90

Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys
95 100 105

Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu
110 115 120

Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val
125 130 135

Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala
140 145 150

Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu
155 160 165

Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp
170 175 180

Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr
185 190 195

Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val
200 205 210

Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly
215 220 225

Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg
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Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly
245 250 255

Leu Thr Leu Ala Phe Lys Ile
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<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

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				20					25					30

Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe
				35					40					45

Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro
				50					55					60

Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys
				65					70					75

Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala
				80					85					90

Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala
				95					100					105

Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp
				110					115					120

Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala
				125					130					135

Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser
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Asp	Asn	Ser	Gly	Leu	Lys	Arg	Lys	Thr	Pro	Ala	Leu	Lys	Met	Ser
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Val	Ser	Lys	Arg	Ala	Arg	Lys	Ala	Ser	Ser	Asp	Leu	Asp	Gln	Ala
				170					175					180
Ser	Val	Ser	Pro	Ser	Glu	Glu	Glu	Asn	Ser	Glu	Ser	Ser	Ser	Glu
				185					190					195
Ser	Glu	Lys	Thr	Ser	Asp	Gln	Asp	Phe	Thr	Pro	Glu	Lys	Lys	Ala
				200					205					210
Ala	Val	Arg	Ala	Pro	Arg	Arg	Gly	Pro	Leu	Gly	Gly	Arg	Lys	Lys
				215					220					225
Lys	Lys	Ala	Pro	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Lys	Ala	Asp	Ser
				230					235					240
Asp	Gly	Ala	Lys	Pro	Glu	Pro	Val	Ala	Met	Ala	Arg	Ser	Ala	Ser
				245					250					255
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Asp	Val	Ser	Val
				260					265					270
Lys	Lys	Pro	Pro	Arg	Gly	Arg	Lys	Pro	Ala	Glu	Lys	Pro	Leu	Pro
				275					280					285
Lys	Pro	Arg	Gly	Arg	Lys	Pro	Lys	Pro	Glu	Arg	Pro	Pro	Ser	Ser
				290					295					300
Ser	Ser	Ser	Asp	Ser	Asp	Ser	Asp	Glu	Val	Asp	Arg	Ile	Ser	Glu
				305					310					315
Trp	Lys	Arg	Arg	Asp	Glu	Ala	Arg	Arg	Arg	Glu	Leu	Glu	Ala	Arg
				320					325					330
Arg	Arg	Arg	Glu	Gln	Glu	Glu	Glu	Leu	Arg	Arg	Leu	Arg	Glu	Gln
				335					340					345
Glu	Lys	Glu	Glu	Lys	Glu	Arg	Arg	Arg	Glu	Arg	Ala	Asp	Arg	Gly
				350					355					360
Glu	Ala	Glu	Arg	Gly	Ser	Gly	Gly	Ser	Ser	Gly	Asp	Glu	Leu	Arg
				365					370					375
Glu	Asp	Asp	Glu	Pro	Val	Lys	Lys	Arg	Gly	Arg	Lys	Gly	Arg	Gly
				380					385					390
Arg	Gly	Pro	Pro	Ser	Ser	Ser	Asp	Ser	Glu	Pro	Glu	Ala	Glu	Leu
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Glu	Arg	Glu	Ala	Lys	Lys	Ser	Ala	Lys	Lys	Pro	Gln	Ser	Ser	Ser
				410					415					420
Thr	Glu	Pro	Ala	Arg	Lys	Pro	Gly	Gln	Lys	Glu	Lys	Arg	Val	Arg
				425					430					435

Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr	440	445	450
Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys	455	460	465
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser	470	475	480
Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg	485	490	495
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser	500	505	510
Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys	515	520	525
Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala	530	535	540
Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile	545	550	555
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys	560	565	570
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala	575	580	585
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	590	595	600
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	605	610	615
Asp	Lys	Glu	His	Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	620	625	630
Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	635	640	645
Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala	650	655	660
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<210> 309

<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

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<210> 310
 <211> 777
 <212> PRT
 <213> Homo sapiens

<400> 310
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 35 40 45
 Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro
 50 55 60
 Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
 65 70 75
 Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

				80					85					90
Phe	Leu	Leu	Ser	Leu 95	Val	Asp	Leu	Asn	Lys 100	Asn	Phe	Lys	Lys	Ile 105
Tyr	Trp	Pro	Ala	Ala 110	Lys	Glu	Arg	Val	Glu 115	Leu	Cys	Lys	Leu	Ala 120
Gly	Lys	Asp	Ala	Asn 125	Thr	Glu	Cys	Ala	Asn 130	Phe	Ile	Arg	Val	Leu 135
Gln	Pro	Tyr	Asn	Lys 140	Thr	His	Ile	Tyr	Val 145	Cys	Gly	Thr	Gly	Ala 150
Phe	His	Pro	Ile	Cys 155	Gly	Tyr	Ile	Asp	Leu 160	Gly	Val	Tyr	Lys	Glu 165
Asp	Ile	Ile	Phe	Lys 170	Leu	Asp	Thr	His	Asn 175	Leu	Glu	Ser	Gly	Arg 180
Leu	Lys	Cys	Pro	Phe 185	Asp	Pro	Gln	Gln	Pro 190	Phe	Ala	Ser	Val	Met 195
Thr	Asp	Glu	Tyr	Leu 200	Tyr	Ser	Gly	Thr	Ala 205	Ser	Asp	Phe	Leu	Gly 210
Lys	Asp	Thr	Ala	Phe 215	Thr	Arg	Ser	Leu	Gly 220	Pro	Thr	His	Asp	His 225
His	Tyr	Ile	Arg	Thr 230	Asp	Ile	Ser	Glu	His 235	Tyr	Trp	Leu	Asn	Gly 240
Ala	Lys	Phe	Ile	Gly 245	Thr	Phe	Phe	Ile	Pro 250	Asp	Thr	Tyr	Asn	Pro 255
Asp	Asp	Asp	Lys	Ile 260	Tyr	Phe	Phe	Phe	Arg 265	Glu	Ser	Ser	Gln	Glu 270
Gly	Ser	Thr	Ser	Asp 275	Lys	Thr	Ile	Leu	Ser 280	Arg	Val	Gly	Arg	Val 285
Cys	Lys	Asn	Asp	Val 290	Gly	Gly	Gln	Arg	Ser 295	Leu	Ile	Asn	Lys	Trp 300
Thr	Thr	Phe	Leu	Lys 305	Ala	Arg	Leu	Ile	Cys 310	Ser	Ile	Pro	Gly	Ser 315
Asp	Gly	Ala	Asp	Thr 320	Tyr	Phe	Asp	Glu	Leu 325	Gln	Asp	Ile	Tyr	Leu 330
Leu	Pro	Thr	Arg	Asp 335	Glu	Arg	Asn	Pro	Val 340	Val	Tyr	Gly	Val	Phe 345
Thr	Thr	Thr	Ser	Ser 350	Ile	Phe	Lys	Gly	Ser 355	Ala	Val	Cys	Val	Tyr 360
Ser	Met	Ala	Asp	Ile 365	Arg	Ala	Val	Phe	Asn 370	Gly	Pro	Tyr	Ala	His 375

300


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<211> 3934
<212> DNA
<213> Homo sapiens

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Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu		20	25	30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala		35	40	45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg		50	55	60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu		65	70	75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala		80	85	90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser		95	100	105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp		110	115	120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu		125	130	135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro		140	145	150
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp		155	160	165
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Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu		185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser		200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu		215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln		230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu		245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly		260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu		275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu		290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala				

305	310	315
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Asp Lys Ala Leu Asp Phe Pro Gly Phe	Leu Asp Met Met Ala Pro	
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 <212> DNA
 <213> Homo sapiens

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4400
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<211> 837
<212> PRT
<213> Homo sapiens

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35 40 45
Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu
50 55 60
Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser
65 70 75
Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu
80 85 90
Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu
95 100 105
Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly
110 115 120
Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp
125 130 135
Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

Val	Thr	Phe	Pro	Gly 440	Lys	Asp	Tyr	Asp	Ala 445	Asp	Arg	Gln	Cys	Gln 450
Leu	Thr	Phe	Gly	Pro 455	Asp	Ser	Arg	His	Cys 460	Pro	Gln	Leu	Pro	Pro 465
Pro	Cys	Ala	Ala	Leu 470	Trp	Cys	Ser	Gly	His 475	Leu	Asn	Gly	His	Ala 480
Met	Cys	Gln	Thr	Lys 485	His	Ser	Pro	Trp	Ala 490	Asp	Gly	Thr	Pro	Cys 495
Gly	Pro	Ala	Gln	Ala 500	Cys	Met	Gly	Gly	Arg 505	Cys	Leu	His	Met	Asp 510
Gln	Leu	Gln	Asp	Phe 515	Asn	Ile	Pro	Gln	Ala 520	Gly	Gly	Trp	Gly	Pro 525
Trp	Gly	Pro	Trp	Gly 530	Asp	Cys	Ser	Arg	Thr 535	Cys	Gly	Gly	Gly	Val 540
Gln	Phe	Ser	Ser	Arg 545	Asp	Cys	Thr	Arg	Pro 550	Val	Pro	Arg	Asn	Gly 555
Gly	Lys	Tyr	Cys	Glu 560	Gly	Arg	Arg	Thr	Arg 565	Phe	Arg	Ser	Cys	Asn 570
Thr	Glu	Asp	Cys	Pro 575	Thr	Gly	Ser	Ala	Leu 580	Thr	Phe	Arg	Glu	Glu 585
Gln	Cys	Ala	Ala	Tyr 590	Asn	His	Arg	Thr	Asp 595	Leu	Phe	Lys	Ser	Phe 600
Pro	Gly	Pro	Met	Asp 605	Trp	Val	Pro	Arg	Tyr 610	Thr	Gly	Val	Ala	Pro 615
Gln	Asp	Gln	Cys	Lys 620	Leu	Thr	Cys	Gln	Ala 625	Arg	Ala	Leu	Gly	Tyr 630
Tyr	Tyr	Val	Leu	Glu 635	Pro	Arg	Val	Val	Asp 640	Gly	Thr	Pro	Cys	Ser 645
Pro	Asp	Ser	Ser	Ser 650	Val	Cys	Val	Gln	Gly 655	Arg	Cys	Ile	His	Ala 660
Gly	Cys	Asp	Arg	Ile 665	Ile	Gly	Ser	Lys	Lys 670	Lys	Phe	Asp	Lys	Cys 675
Met	Val	Cys	Gly	Gly 680	Asp	Gly	Ser	Gly	Cys 685	Ser	Lys	Gln	Ser	Gly 690
Ser	Phe	Arg	Lys	Phe 695	Arg	Tyr	Gly	Tyr	Asn 700	Asn	Val	Val	Thr	Ile 705
Pro	Ala	Gly	Ala	Thr 710	His	Ile	Leu	Val	Arg 715	Gln	Gln	Gly	Asn	Pro 720
Gly	His	Arg	Ser	Ile	Tyr	Leu	Ala	Leu	Lys	Leu	Pro	Asp	Gly	Ser

	725		730		735									
Tyr	Ala	Leu	Asn	Gly	Glu	Tyr	Thr	Leu	Met	Pro	Ser	Pro	Thr	Asp
				740					745					750
Val	Val	Leu	Pro	Gly	Ala	Val	Ser	Leu	Arg	Tyr	Ser	Gly	Ala	Thr
				755					760					765
Ala	Ala	Ser	Glu	Thr	Leu	Ser	Gly	His	Gly	Pro	Leu	Ala	Gln	Pro
				770					775					780
Leu	Thr	Leu	Gln	Val	Leu	Val	Ala	Gly	Asn	Pro	Gln	Asp	Thr	Arg
				785					790					795
Leu	Arg	Tyr	Ser	Phe	Phe	Val	Pro	Arg	Pro	Thr	Pro	Ser	Thr	Pro
				800					805					810
Arg	Pro	Thr	Pro	Gln	Asp	Trp	Leu	His	Arg	Arg	Ala	Gln	Ile	Leu
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Glu	Ile	Leu	Arg	Arg	Arg	Pro	Trp	Ala	Gly	Arg	Lys			
				830					835					

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- <211> 23
- <212> DNA
- <213> Artificial
- <220>
- <221> Artificial Sequence
- <222> 1-23
- <223> Synthetic construct.
- <400> 318
- ccctgaagct gccagatggc tcc 23
- <210> 319
- <211> 24
- <212> DNA
- <213> Artificial
- <220>
- <221> Artificial Sequence
- <222> 1-24
- <223> Synthetic construct.
- <400> 319
- ctgtgctctt cggtgcagcc agtc 24
- <210> 320
- <211> 43
- <212> DNA
- <213> Artificial
- <220>
- <221> Artificial Sequence
- <222> 1-43
- <223> Synthetic construct.

<400> 320
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<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

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ttgtggactg gtgtttggta tcttgccct aactctaatt gtcctgtttt 200
gggggagcaa gcacttctgg ccggaggtag ccaaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
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gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
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ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550
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<210> 322

<211> 317
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys
 50 55 60
 Ala Tyr Asp Met Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys
 65 70 75
 Lys Ile Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe
 80 85 90
 Arg Ser Gly Asn Gly Thr Asp Glu Thr Leu Glu Val His Asp Phe
 95 100 105
 Lys Asn Gly Tyr Thr Gly Ile Tyr Phe Val Gly Leu Gln Lys Cys
 110 115 120
 Phe Ile Lys Thr Gln Ile Lys Val Ile Pro Glu Phe Ser Glu Pro
 125 130 135
 Glu Glu Glu Ile Asp Glu Asn Glu Glu Ile Thr Thr Thr Phe Phe
 140 145 150
 Glu Gln Ser Val Ile Trp Val Pro Ala Glu Lys Pro Ile Glu Asn
 155 160 165
 Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu Ile Cys Asp Asn
 170 175 180
 Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser Val Ser Glu
 185 190 195
 Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe Pro Ala
 200 205 210
 Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val Pro
 215 220 225
 Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu
 230 235 240
 Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe
 245 250 255
 Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg
 260 265 270

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
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Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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tggaaccacca acgacgtggc gcgaacttc tacaaccgcg tgcgtgccag 550
cggcatgaag tttagattg gccaggccct gtacctgggc ttcattctct 600
cgtccctctc gctcattggc ggaccctgc tttgcctgtc ctgccaggac 650
gaggcaccct acaggcccta ccaggccccg cccaggggcca ccacgaccac 700
tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750
gggccccctc agtgacctc gccacgcaca gcgggtacag gctgaacgac 800
tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850
gtccccggcg ggactgtcaa tggaggcagg ggttcacagc caaagtttac 900
ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaatgt 950
cttagagca caggacaga gggggaaata agaggaggag aaagctctct 1000

ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050
 atatttatgt ggggtgatttg ataacaagtt taatataaag tgacttggga 1100
 gtttggtcag tgggggttgggt ttgtgatcca ggaataaacc ttgcggatgt 1150
 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 324
 Met Ala Ser Thr Ala Val Gln Leu Leu Gly Phe Leu Leu Ser Phe
 1 5 10 15
 Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp
 20 25 30
 Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser
 35 40 45
 Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly
 50 55 60
 Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln
 65 70 75
 Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu
 80 85 90
 Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu
 110 115 120
 Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala
 125 130 135
 Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro
 140 145 150
 Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr
 155 160 165
 Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu
 170 175 180
 Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln
 185 190 195
 Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala
 200 205 210
 Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val
 215 220 225

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
 230 235

<210> 325
 <211> 2121
 <212> DNA
 <213> Homo sapiens

<400> 325
 gagctcccct caggagcgcg ttagcttcac accttcggca gcaggagggc 50
 ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac 100
 cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150
 gcacgcgggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200
 aaccccgta cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
 gacttcacgc catgctgcag gcagtgcgag ccctgatgat cgtaggcatc 350
 gtcctgggtg ccattggcct cctggatatcc atctttgccc tgaaatgcat 400
 ccgcattggc agcatggagg actctgcaa agccaacatg aactgacct 450
 ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500
 gtgtttgcca acatgctggg gactaacttc tggatgtcca cagctaacat 550
 gtacaccggc atgggtggga tggcgcagac tgttcagacc aggtacacat 600
 ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650
 ggggggtgta tgatgtgcat cgcctgccg ggcctggcac cagaagaaac 700
 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750
 agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800
 aagaagatat acgatggagg tgccgcaca gaggacgagg tacaatctta 850
 tccttccaag cagcactatg tgtaatgctc taagacctct cagcacgggc 900
 ggaagaaact ccgggagagc tcacccaaaa aacaaggaga tcccatctag 950
 atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000
 catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050
 ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100
 attttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150
 gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200
 cccctcttc ctctagtca ataaacccat tgatgatcta tttccagct 1250

tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300
 ttctgctgtt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350
 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400
 cccatgatct cggtttttctt aactgtgat cttaaaagtt accaaaccaa 1450
 agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500
 tcttattaca gcaacaccat tctaggagtt tcctgagctc tccactggag 1550
 tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600
 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650
 taaaatgata cactatctct gtgaaatagc ctcacccta catgtggata 1700
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950
 gaggtgagg tgggaggatc acttgagccc agggagggtg gggctgcagt 2000
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
 gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100
 aggttaaaac taattcttta a 2121

<210> 326
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 326
 Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile
 1 5 10 15
 Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp
 20 25 30
 Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
 35 40 45
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
 50 55 60
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
 65 70 75
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

	80	85	90
Ala Ile Gly Leu	Leu Val Ser Ile Phe	Ala Leu Lys Cys Ile Arg	
	95	100	105
Ile Gly Ser Met	Glu Asp Ser Ala Lys	Ala Asn Met Thr Leu Thr	
	110	115	120
Ser Gly Ile Met	Phe Ile Val Ser Gly	Leu Cys Ala Ile Ala Gly	
	125	130	135
Val Ser Val Phe	Ala Asn Met Leu Val	Thr Asn Phe Trp Met Ser	
	140	145	150
Thr Ala Asn Met	Tyr Thr Gly Met Gly	Gly Met Val Gln Thr Val	
	155	160	165
Gln Thr Arg Tyr	Thr Phe Gly Ala Ala	Leu Phe Val Gly Trp Val	
	170	175	180
Ala Gly Gly Leu	Thr Leu Ile Gly Gly	Val Met Met Cys Ile Ala	
	185	190	195
Cys Arg Gly Leu	Ala Pro Glu Glu Thr	Asn Tyr Lys Ala Val Ser	
	200	205	210
Tyr His Ala Ser	Gly His Ser Val Ala	Tyr Lys Pro Gly Gly Phe	
	215	220	225
Lys Ala Ser Thr	Gly Phe Gly Ser Asn	Thr Lys Asn Lys Lys Ile	
	230	235	240
Tyr Asp Gly Gly	Ala Arg Thr Glu Asp	Glu Val Gln Ser Tyr Pro	
	245	250	255
Ser Lys His Asp	Tyr Val		
	260		

<210> 327
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<400> 327
 ggaaaaactg ttctcttctg tggcacagag aaccctgctt caaagcagaa 50
 gtagcagttc cggagtccag ctggctaaaa ctcatcccag aggataatgg 100
 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaatg 150
 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgtcggcctt 200
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
 tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350

tgctgcttcc gtgatgtcct tcttggttt catgatggcc atccttggca 400
 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450
 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600
 tggaccacgg cactggtgct gattgttgga ggagctctgt tctgctgct 650
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700
 atcgcacaa ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750
 tactccagaa gtcagtatgt gtagtttgt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tactttctca aaatggaccc 850
 caaagaaact ttgatttact gttcttaact gcctaatttt aattacagga 900
 actgtgcac agctatttat gattctataa gctatttcag cagaatgaga 950
 tattaaacct aatgctttga ttgttctaga aagtatagta atttgttttc 1000
 taaggtggtt caagcatcta ctctttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattatct tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgt acatttatat ctacataga gacatgotta 1150
 tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200
 actcaactat tgcttttcag ggaaatcatg gataggggtg aagaagggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcttc cattttataat 1300
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400
 atcctcttct ccagagggt ttttttttct tgtgtattaa attaacattt 1450
 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550
 gttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650
 gagtacagac tttgagggtt catcaatata aataaaagag cagaaaaata 1700
 tgtcttggtt ttcatgtgt taccaaaaaa acaacaacaa aaaaagtgtg 1750
 cctttgagaa cttcacctgc tctatgtgg gtacctgagt caaaattgtc 1800

Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215				220						225

<210> 329
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<400> 329
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 ctgggctggg tgaatggcct ggtctcctgt gccctgccca tgtggaaggt 100
 gaccgctttc atcggcaaca gcacgtggtt ggcccaggtg gtgtgggagg 150
 gcctgtggat gtcttgcgtg gtgcagagca ccggccagat gcagtgcaag 200
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
 cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300
 ttgtctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350
 cgcttgggtc tcacctctgg gattgtcttt gtcattctcag gggtcctgac 400
 gctaataccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
 accccctggg ggctgaggcc caaaagcggg agctgggggc ctccctctac 500
 ttgggctggg cggcctcagg cttttgttg ctgggtgggg ggttgctgtg 550
 ctgcacttgc ccctoggggg ggtcccaggg cccagccat tacatggccc 600
 gctactcaac atctgccct gccatctctc gggggccctc tgagtaccct 650
 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700
 gagccatcca gaagtggcag tgcccaacag ctttgggatg ggttcgtacc 750
 ttttgtttct gcctcctgct atttttcttt tgactgagga tatttaaaat 800
 tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850
 gctgtttctc acccttggat gatggagcca aagaggggat gctttgagat 900
 tctggatctt gacatgccca tcttagaagc cagtcaagct atggaactaa 950
 tgcggagggt gcttgctgtg ctggctttgc aacaagacag actgtcccca 1000
 agagttcctg ctgctgctgg gggctgggct tccctagatg tcaactggaca 1050
 gctgcccccc atcctactca ggtctctgga gtcctctct tcacccttg 1100
 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150
 cctctgtttc ctccgtcctg ataagacgtc cccccccag ggccaggtcc 1200
 cagctatgta gacccccgcc cccacctcca aactgcacc cttctgccct 1250

gccccctcg tctcaccccc tttaactca catttttatc aaataaagca 1300

tgttttgta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
1				5					10					15

Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
				215					220

<210> 331

<211> 1160

<212> DNA

1	5	10	15
Tyr Ser Ser Leu	Leu Ala Leu Pro Pro	Ala Leu Glu Thr Ala	Arg
	20	25	30
Ala Leu Met Cys Val	Ala Val Ala Leu Ser Leu	Ile Ala Leu Leu	
	35	40	45
Ile Gly Ile Cys Gly	Met Lys Gln Val Gln Cys Thr	Gly Ser Asn	
	50	55	60
Glu Arg Ala Lys Ala	Tyr Leu Leu Gly Thr Ser Gly	Val Leu Phe	
	65	70	75
Ile Leu Thr Gly Ile	Phe Val Leu Ile Pro Val Ser	Trp Thr Ala	
	80	85	90
Asn Ile Ile Ile Arg	Asp Phe Tyr Asn Pro Ala Ile	His Ile Gly	
	95	100	105
Gln Lys Arg Glu Leu	Gly Ala Ala Leu Phe Leu Gly	Trp Ala Ser	
	110	115	120
Ala Ala Val Leu Phe	Ile Gly Gly Gly Leu Leu Cys	Gly Phe Cys	
	125	130	135
Cys Cys Asn Arg Lys	Lys Gln Gly Tyr Arg Tyr Pro	Val Pro Gly	
	140	145	150
Tyr Arg Val Pro His	Thr Asp Lys Arg Arg Asn Thr	Thr Met Leu	
	155	160	165
Ser Lys Thr Ser Thr	Ser Tyr Val		
	170		

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
 agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50
 atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100
 ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
 agaagtatcc agtgggtggc atcccctgcc ccatcacata cctaccagtt 200
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
 aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
 tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400
 ggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
1 5 10 15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

cccgcgcccg gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50

ctgctcgcgc cccgccgcca tggctgcctc ccccgcgagg cctgctgtcc 100

tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150

ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200

tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaatth gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattggtc cccggagccc ctacggcttt aggcatggag ccagcgtcaa 500

ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550

agcgattctc ttcattgtatc tcctaagtcc ttacactact tggtttctga 600

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
gaagagttaa aacaacacat gtaaatgcct tttgatattt catgggaatg 700
cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
<211> 148
<212> PRT
<213> Homo sapiens

<400> 336
Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
1 5 10 15
Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
20 25 30
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
35 40 45
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
50 55 60
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
65 70 75
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
80 85 90
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
95 100 105
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
110 115 120
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
125 130 135
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
140 145

<210> 337
<211> 1310
<212> DNA
<213> Homo sapiens

<400> 337
cggctcgagc ccgcccggaa gtgcccagg ggccgcgatg gagctggggg 50
agccgggagc tcggtagcgc ggcgggcaag gcaggcgcca tgaccctgat 100
tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgctgcc 150
ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200
gaccactgc ccagccgctc agggaccca acgcatccc agccagcgc 250

Thr Pro Thr Pro Ser Gln Pro Ser Ala Ala Met Ala Ala Thr Asp
50 60

Ser Met Arg Gly Glu Ala Pro Gly Ala Glu Thr Pro Ser Leu Arg
65 75

His Arg Gly Gln Ala Ala Gln Pro Glu Pro Ser Thr Gly Phe Thr
80 90

Ala Thr Pro Pro Ala Pro Asp Ser Pro Gln Glu Pro Leu Val Leu
95 105

Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp
110 120

Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly
125 135

Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly
140 150

Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys
155 165

Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro
170 180

Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile
185 195

Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu
200 210

Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala
215 225

Thr Leu Gly Leu Ala Gly Phe Thr Leu Leu Leu Ser Leu Leu Ala
230 240

Phe Ala Met Tyr Arg Pro
245

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

gagattggaa acagccaggt tggagcagtg agtgagtaag gaaacctggc 50

tgccctctcc agattcccca ggctctcaga gaagatcagc agaaagtctg 100

caagacccta agaaccatca gccctcagct gcacctcctc ccctccaagg 150

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tcaggccagc ctcatcagtc gctgtgactt ggcccagggtg ctgcagctgg 250

<210> 341
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 341
 ccctccaagg atgacaaagg cgc 23

<210> 342
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-29
 <223> Synthetic construct.

<400> 342
 ggtcagcagc tttcttgccc taaatcagg 29

<210> 343
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 343
 atctcaggcg gcacacctgtc agcc 24

<210> 344
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 344
 gtggatgcct gcaagaagggt tggg 24

<210> 345
 <211> 45
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 345
agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346
<211> 2575
<212> DNA
<213> Homo sapiens

<400> 346
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aaggagaaaa ccggggtaaa gggagggaa caattcaatt tgaagtcctt 200
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300
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<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

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Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

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Gly Ser Pro Gln His Leu Cys Phe Ala	Val Arg Gln Glu Gln Val	
560	565	570
Ile Leu Gln Asn Cys Thr Glu Glu Gly	Leu Ala Ile His Gln Gln	
575	580	585
His Trp Asp Phe Gln Glu Asn Gly Met	Ile Val His Ile Leu Ser	
590	595	600
Gly Lys Cys Met Glu Ala Val Val Gln	Glu Asn Asn Lys Asp Leu	
605	610	615
Tyr Leu Arg Pro Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg Phe	
620	625	630
Asp Gln Ile Asn Ala Val Asp Glu Arg		
635		

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<210> 348
 <211> 23
 <212> DNA
 <213> Artificial

 <220>
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 <222> 1-23
 <223> Synthetic construct.

 <400> 348
 ggagaggtgg tggccatgga cag 23

 <210> 349
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 349
 ctgtcactgc aaggagccaa cacc 24

 <210> 350
 <211> 45
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

 <400> 350
 tatgtcgctg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351
<211> 2524
<212> DNA
<213> Homo sapiens

<400> 351
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ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100
tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150
tcttcatcct cccctogaac cccaccagcc ccagcccgcc ccccggtgtgc 200
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cctggcactg cacccccagc caccocatca ggctttgagg aggggccgcc 350
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<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

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20 25 30

Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
35 40 45

Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60

Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75

Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90

Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105

Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120

Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
200 205 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
215 220 225

Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
230 235 240

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

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tccgggggttc tggcccctgc ggtgctcaca gacgatgttc cacaggagcc 150
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<210> 354
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 354
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser
 1 5 10 15
 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu
 20 25 30
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
 35 40 45
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
 50 55 60
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
 65 70 75
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
 80 85 90
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
 95 100 105
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
 110 115 120

Ser

<210> 355
 <211> 2134
 <212> DNA
 <213> Homo sapiens

<400> 355
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gtgcctgacg gcggcgctgg cccacggctg tctgcaactg cacagcaact 150
tctccaagaa gttctccttc taccgccacc atgtgaactt caagtccctg 200
tggttggtggc acatccccgt gtcaggggag ctgctcaccg actggagcga 250
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140

145

150

Ser Pro Arg Gly Asp Leu Pro
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<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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ttgagaaatc ctcatatggt cctggtgctg cccaggaacc caogtggctc 150
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
cataggcttc ttccaggatt tagaaatacc agcagtgtccc atactccata 250
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gaggtttctga cacactacaa catcactggg aacaccatct gcctctttcg 350
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<210> 358
<211> 273
<212> PRT
<213> Homo sapiens

<400> 358
Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu
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Thr Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser
20 25 30
Ser Asp Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp
35 40 45
Val Pro Ala Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val
50 55 60
Ile Gly Phe Phe Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu
65 70 75
His Ser Met Val Gln Lys Phe Pro Gly Val Ser Phe Gly Ile Ser
80 85 90
Thr Asp Ser Glu Val Leu Thr His Tyr Asn Ile Thr Gly Asn Thr
95 100 105
Ile Cys Leu Phe Arg Leu Val Asp Asn Glu Gln Leu Asn Leu Glu
110 115 120
Asp Glu Asp Ile Glu Ser Ile Asp Ala Thr Lys Leu Ser Arg Phe
125 130 135
Ile Glu Ile Asn Ser Leu His Met Val Thr Glu Tyr Asn Pro Val
140 145 150
Thr Val Ile Gly Leu Phe Asn Ser Val Ile Gln Ile His Leu Leu
155 160 165
Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu Glu Asn Met His
170 175 180
Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys Ile Leu Phe
185 190 195

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser	
				200					205					210	
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr	
				215					220					225	
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val	
				230					235					240	
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly	
				245					250					255	
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys	
				260					265					270	

Val Glu Leu

```

<210> 359
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 359
ccagcagtgc ccatactcca tagc 24

<210> 360
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 360
tgacgagtgg gatacactgc 20

<210> 361
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 361
gctctacgga aacttctgct gtgg 24

<210> 362

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<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50
ccggcgcggg tggcggagag atcagaagcc tcttcccaa gccgagccaa 100
cctcagcggg gaccgaggct cagggaacgc gcggcgccgg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgctggc tgtggctcgg gctggcgccg gcgcttgggc 250
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca aggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcgggttga cctcagtcct ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450
cttggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
cctggacaca ttaggctcta tgcgtagaa aaagagaatt tgctgtgtt 650
tccagtttgg gtagtggtgg gcatagttac tgctgtggc ctaggtctca 700
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850
tgccttctgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900
tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgcggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050
atgtagcctt ggagacccag gcaaggacaa gtacacgtgt actcacagag 1100
ggagagaaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150
cctgatatga ggagccagtg ttgcatgatg aaaagatggg atgattctac 1200
atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250
caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300
tgccttaatg gagacaatag cagatcctgt agtattttcca gtagacatgg 1350
ccttttaatc taagggctta agactgatta gtcttagcat ttactgtagt 1400
tggaggatgg agatgctatg atggaagcat acccaggggtg gccttttagca 1450
cagtatcagt accatttatt tgtctgccgc ttttaaaaaa taccatttgg 1500
ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550
aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600
tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650
attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700
tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750
cgtggagagt aaaaagtatc ggtttta 1777

<210> 364
<211> 269
<212> PRT
<213> Homo sapiens

<400> 364
Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
1 5 10 15
Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
20 25 30
Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
35 40 45
Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
50 55 60
Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
65 70 75
Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
80 85 90
Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
95 100 105

cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
cogaattccc agaaaaagaa tatgaagggtg aaaagggtttc tgtcacaaca 650
agattactga tttcccattt aagtggaatt cgtcattatg aaaaggacat 700
aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
agaatggttc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
gattttacta aattttaaac agagcaggag aatgaagcca aatgccggaa 850
ttcaaaacct ggcaagaaaa agaattgattt tgaacaaggc gaattatatt 900
tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaaat 950
gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000
ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050
tggaactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
caggaagaaa acgagccagt gatttacaat agagcaagggt aatgaatac 1150
cttctgctgt gtctagctat atcgcatctt aacactatctt tattaattaa 1200
aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250
gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300
catgtttata aagtaaaaaa a 1321

<210> 366
<211> 373
<212> PRT
<213> Homo sapiens

<400> 366
Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro
1 5 10 15
Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
20 25 30
Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
35 40 45
Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
50 55 60
Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu
65 70 75
Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro
80 85 90

<211> 30
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
tggaagagaa gtctgggtcag aaggttttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttggttt cattctcctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaacctcag aacaactcat tttgcacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtogca tgcacgcgta cgtaagctcg 50

gaattcggct	cgaggctggt	gggaagaagc	cgagatggcg	gcagccagcg	100
ctggggcaac	ccggctgctc	ctgctcttgc	tgatggcggg	agcagcgccc	150
agtcgagccc	ggggcagcgg	ctgccggggc	gggactgggt	cgcgaggggg	200
tggggcgga	ggtcgagagg	gcgaggcctg	tggcacgggt	gggctgctgc	250
tggagcactc	atttgagatc	gatgacagtg	ccaacttccg	gaagcggggc	300
tactgctct	ggaaccagca	ggatggtacc	ttgtccctgt	cacagcggca	350
gctcagcgag	gaggagcggg	gccgactccg	ggatgtggca	gccctgaatg	400
gcctgtaccg	ggtccggatc	ccaaggcgac	ccggggccct	ggatggcctg	450
gaagctgggt	gctatgtctc	ctcctttgtc	cctgcgtgct	ccctggtgga	500
gtcgcacctg	tccgaccagc	tgaccctgca	cgtggatgtg	gccggcaacg	550
tgggtggcgt	gtcggtggtg	acgcaccccg	ggggctgccg	gggccatgag	600
gtggaggacg	tggacctgga	gctgttcaac	acctcgggtg	agctgcagcc	650
gcccaccaca	gccccaggcc	ctgagacggc	ggccttcatt	gagcgcctgg	700
agatggaaca	ggcccagaag	gccaagaacc	cccaggagca	gaagtccttc	750
ttcgccaaat	actggatgta	catcattccc	gtcgtcctgt	tcctcatgat	800
gtcaggagcg	ccagacaccg	ggggccaggg	tgggggtggg	ggtgggggtg	850
gtggtggggg	tagtggcctt	tgctgtgtgc	caccctccct	gtaagtctat	900
ttaaaaaacat	cgacgataca	ttgaaatgtg	tgaacgtttt	gaaaagctac	950
agcttccagc	agccaaaagc	aactgtttgt	ttggcaagac	ggtcctgatg	1000
tacaagcttg	attgaaattc	actgctcact	tgatacgtta	ttcagaaacc	1050
caaggaatgg	ctgtcccat	cctcatgtgg	ctgtgtggag	ctcagctgtg	1100
ttgtgtggca	gtttattaaa	ctgtccccc	gatcgacacg	caaaaaaaaa	1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met Ala Ala Ala Ser Ala Gly Ala Thr Arg Leu Leu Leu Leu Leu
1 5 10 15

Leu Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys
20 25 30

Arg Ala Gly Thr Gly Ala Arg Gly Ala Gly Ala Glu Gly Arg Glu
35 40 45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373
 <211> 1706
 <212> DNA
 <213> Homo sapiens

<400> 373
 ggagcgtgc tggaaccgga gccggagccg gagccacagc ggggagggtg 50
 gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100
 cagcaggtcg tccgggggcc caccatgctg gtgactgcct accttgcttt 150
 tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200

ctctgtgtta ctccattta gaaaataaac actttttaaat gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser
1				5					10					15

Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly
				20					25					30

Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe
				35					40					45

Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala
				50					55					60

Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly
				65					70					75

Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu
				80					85					90

Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys
				95					100					105

Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu
				110					115					120

Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala
				125					130					135

Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala
				140					145					150

Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu
				155					160					165

Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val
				170					175					180

Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp
				185					190					195

Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu
				200					205					210

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn
				215					220					225

Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu
				230					235					240

Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile	245	250	255
Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp	260	265	270
Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe	275	280	285
Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg	290	295	300
Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu	305	310	315
Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr	320	325	330
Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile	335	340	345
Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser	350	355	360
Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala	365	370	375
Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys	380	385	390
Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr	395	400	405
Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu	410	415	420
Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu	425	430	435
Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu	440	445	450

<210> 375
 <211> 1098
 <212> DNA
 <213> Artificial

<400> 375
 gcgacgcgcg gcggggcggc gagaggaaac gcggcgcccg gccgggcccg 50
 gccctggaga tgggtccccg cgccgcgggc tgggtgtgtc tcgtgctctg 100
 gctccccgcg tgcgtcgcg cccacggctt ccgtatccat gattatttgt 150
 actttcaagt gotgagtcct ggggacattc gatacatctt cacagccaca 200
 cctgccaaagg actttgggtg tatctttcac acaaggtatg agcagattca 250

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
 95 100 105
 Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
 110 115 120
 Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
 125 130 135
 Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
 140 145 150
 Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
 155 160 165
 Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
 170 175 180
 Leu Gln Pro Pro Trp Thr Phe Trp
 185

<210> 377
 <211> 496
 <212> DNA
 <213> Artificial

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50
 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctctccta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
 aagaccaggg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20						25					30
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35						40					45
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50						55					60
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65						70					75
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80						85					90
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95						100					105
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu				
				110					115					

<210> 379
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 379
 ctgcctccac tgctctgtgc tggg 24

 <210> 380
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 380
 cagagcagtg gatgttcccc tggg 24

 <210> 381
 <211> 45
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-45

<223> Synthetic construct.

<400> 381
ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382
<211> 764
<212> DNA
<213> Homo sapiens

<400> 382
ctcgcttctt ctttctggat gggggcccag gggggcccagg agagtataaa 50
ggcgatgtgg aggggtgccc gcacaaccag acgcccagtc acaggcgaga 100
gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150
ctcctggggg gccccacctg ggcagggaag atgtatggcc ctggaggagg 200
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccagggt gaaacttgga 300
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
ctttcctccg gggtatggtc atgtacacca gcaaggaccg ctatttctat 450
tttgggaagc ttgatggcca gatctcctct gcctacccca gccaagaggg 500
gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcatcaaga 550
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
ccagttaatc tcacatactc agcaaactca cccgtgggtc gctagggtgg 650
ggtatggggc catccgagct gaggccatct gtgtgggtgg ggctgatggg 700
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
gcttctgcag aaaa 764

<210> 383
<211> 178
<212> PRT
<213> Homo sapiens

<400> 383
Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu
1 5 10 15
Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly
20 25 30
Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr
35 40 45

Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln
				50					55					60
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly
				65					70					75
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr
				80					85					90
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met
				95					100					105
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly
				110					115					120
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val
				125					130					135
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly
				140					145					150
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro
				155					160					165
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg		
				170					175					

<210> 384
 <211> 2379
 <212> DNA
 <213> Homo sapiens

<400> 384
 gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50
 agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100
 atacagatgt ggcagctcag gtagcccaa attgcctgga agaatacatc 150
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
 cccctcccca cccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250
 atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300
 tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350
 atgttcctaaa atcgggtccat ctccaagggt gtccaatttt tcttcctggg 400
 tgtcagcgag cctgactca ctacagtgc gctgacagg gctgtcatgc 450
 aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
 acaaaggatg gggttcaatg taattaggct actgagcgga tcagctgtag 550
 cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600
 cgaggatgcc ctaagggtgt taggtgtgaa ggcaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tatactctgct ggttgcttag 700
gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750
aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800
caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
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gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
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cgctcaacc tggattccaa caagctcaca ttatttggtc aagagatttt 1400
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agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600
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gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000
gggaccctgc acctataaca aatcgggtc cagggagtgt gaggtatgaa 2050
ccattgtgat aaaaagagct cttaaaagct gggaaataag tggtgcttta 2100

ttgaactctg gtgactatca aggggaacgcg atgccccccc tccccttccc 2150
 tctccctctc actttggtgg caagatcctt ccttgtccgt tttagtgcac 2200
 tcataatact gggtcattttc ctctcatata taatcaaccc attgaaattt 2250
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385
 <211> 513
 <212> PRT
 <213> Homo sapiens

<400> 385
 Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala
 1 5 10 15
 Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala
 20 25 30
 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
 35 40 45
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
 50 55 60
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
 65 70 75
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
 80 85 90
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
 95 100 105
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
 110 115 120
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
 125 130 135
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
 140 145 150
 Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
 155 160 165
 Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
 170 175 180
 Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
 185 190 195
 Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu

200	205	210
His Leu Glu His	Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu Phe
215	220	225
Pro Arg Leu Val	Ser Leu Gln Asn Leu	Tyr Leu Gln Trp Asn Lys
230	235	240
Ile Ser Val Ile	Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser Leu
245	250	255
Gln Arg Leu Asp	Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser Gly
260	265	270
Pro Ser Val Phe	Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn Leu
275	280	285
Asp Ser Asn Lys	Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp Ser
290	295	300
Trp Ile Ser Leu	Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp Glu
305	310	315
Cys Ser Arg Asn	Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser Phe
320	325	330
Lys Gly Leu Arg	Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys Glu
335	340	345
Leu Gln Gly Val	Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser Ile
350	355	360
Cys Gly Lys Ser	Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala Leu
365	370	375
Pro Lys Pro Thr	Phe Lys Pro Lys Leu	Pro Arg Pro Lys His Glu
380	385	390
Ser Lys Pro Pro	Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro Gly
395	400	405
Pro Glu Thr Asp	Ala Asp Ala Glu His	Ile Ser Phe His Lys Ile
410	415	420
Ile Ala Gly Ser	Val Ala Leu Phe Leu	Ser Val Leu Val Ile Leu
425	430	435
Leu Val Ile Tyr	Val Ser Trp Lys Arg	Tyr Pro Ala Ser Met Lys
440	445	450
Gln Leu Gln Gln	Arg Ser Leu Met Arg	Arg His Arg Lys Lys Lys
455	460	465
Arg Gln Ser Leu	Lys Gln Met Thr Pro	Ser Thr Gln Glu Phe Tyr
470	475	480
Val Asp Tyr Lys	Pro Thr Asn Thr Glu	Thr Ser Glu Met Leu Leu
485	490	495

Asn	Gly	Thr	Gly	Pro	Cys	Thr	Tyr	Asn	Lys	Ser	Gly	Ser	Arg	Glu
				500					505					510

Cys Glu Val

<210> 386
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 386
 ctgggatctg aacagtttcg gggc 24

<210> 387
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 387
 ggtccccagg acatggtctg tccc 24

<210> 388
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

<400> 388
 gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
 <211> 1449
 <212> DNA
 <213> Homo sapiens

<400> 389
 agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
 ttgactgtcc tttaaatatg tcaagatcca gactttttcag tgtcacctca 100
 gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150
 ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctgggat atctggatcc tctgctgct ggttttgggtg 250
 gcagctcttc tctgtggagc tgtgggtcctc tgccctccagt gctgggtgag 300
 gagaccccgga attgattctc acaggcgcac catgggcagtt tttgctgttg 350
 gagacttgga ctctatttat gggacagaag cagctgtgag tccaactggt 400
 ggaattcacc ttcaaactca aaccctgac ctatatcctg ttctgctcc 450
 atgttttggc cctttaggct cccacctcc atatgaagaa attgtaaaaa 500
 caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
 taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
 tccagagatc tattcatata gtctgaggaa ggacaattcg aaaaaagaat 650
 ggatgttgga aaaaattttg gtcatggaga tgtttaaata gttaaagtagc 700
 aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750
 attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
 gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850
 tctgctttaa actctttcct agcatggggt ccataaaaat tattataatt 900
 taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950
 agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
 tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
 gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100
 tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150
 ccaacacggg gagaaaagaa aatttcccct ttacagtaa tgaatgtggc 1200
 ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250
 cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
 gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
 agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
 ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
1				5				10					15	

Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
				20					25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
			50						55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
			65						70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
				80					85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
				95					100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
				110					115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
				125					130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
				140					145						

<210> 391
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 391
 cttttcagtg tcacctcagc gatctc 26

 <210> 392
 <211> 23
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

 <400> 392
 ccaaaacatg gagcaggaac agg 23

 <210> 393
 <211> 47
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50
accacacggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100
gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
tctctttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300
cttgcgtgaag atgaagaata tacaatattg aggatatttt tttctttttt 350
ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
tatgtcccag aaattgagtt tactgttgct tgtatttggga ctcatattggg 500
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550
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attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750
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tgtacataaa aatttttaaag ttatttgttt gctttcaggc aagtctgttc 1050
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggg 1100

Leu	Leu	Leu	Leu	Val	Phe	Gly	Leu	Ile	Trp	Gly	Leu	Met	Leu	Leu	20	25	30
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu	35	40	45
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu	50	55	60
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser	65	70	75
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu	80	85	90
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp	95	100	105
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr	110	115	120
Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val	125	130	135
Ser	Gly	Ser	Ile	Arg											140		

<210> 396
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 396
 cgcgccggg cgcgcggggt gagcgtgccg aggcggctgt ggcgaggct 50
 tccagcccc accatgccgt ggcccctgct gctgctgctg gccgtgagtg 100
 gggcccagac aaccggcca tgcttccccg ggtgccaatg cgaggtggag 150
 accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200
 cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250
 tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300
 gggccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350
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atgggaaccc tctagctgtc attggtccgg gtgccttcgc ggggctggga 750
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aacagactgc tgtcctgggc tgcctcaggt cccgagtaac ttatgttcaa 1200
tgtgccaaca ccagtgggga gcccgaggc ctatgtggca gcgtcaccac 1250
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tcttttctaa catagccctt tctttgccat gaggccatga ggcccgcttc 1600
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tcaagtccac ccttctcatg tgacagatgg ggaaactgag gccttgagaa 1700
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cattagcaca ggagtagcag cagcaggaca ggcaagagcc tcacaagtgg 1900
gactctgggc ctctgaccag ctgtgcggca tgggctaagt cactctgcc 1950
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gagcctcatc tggctgggat ctccaagggg cctcctggat tcagtcccca 2150
 ctggccctga gcacgacagc ccttcttacc ctcccaggaa tgccgtgaaa 2200
 ggagacaagg tctgcccagc ccatgtctat gctctacccc cagggcagca 2250
 tctcagcttc cgaaccctgg gctgtttcct tagtcttcat tttataaaag 2300
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 gctggccggg gatggagaca tgtcatttgt aaaagcagaa aaaggttgca 2400
 tttgttcaact tttgtaatat tgtcctgggc ctgtgttggg gtgttggggg 2450
 aagctgggca tcagtggcca catgggcatc aggggctggc cccacagaga 2500
 cccacaggg cagtgaagctc tgtcttcccc cacctgccta gcccatcatc 2550
 tatctaaccg gtccttgatt taataaacac tataaaaggt ttaaaaaaaaa 2600
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Leu	Ala	Val	Ser	Gly	Ala	Gln
1				5					10					15

Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr
				20					25					30

Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser
				35					40					45

Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr
				50					55					60

Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu
				65					70					75

Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp
				80					85					90

Leu	Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe	Ser
				95					100					105

Arg	Leu	Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu
				110					115					120

Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser	Asp
				125					130					135

Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala
				140					145					150

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgag ccacagcttc tgtgagattc gattttotccc cagttcccct 50

gtgggtctga ggggaccaga agggtagct acgttggctt tctggaagg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150

atgtcattct ctatctattc actgcaagt cctgctgttc caggcottac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaacctt caggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600

tgctgcctcc tgcgccattt gctaagactc tatctggaca gggatattta 650

aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700

ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgcccac 750

atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800
gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850
gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
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atTTTTgtaa tatctttctg ctattggata tttttattag ttaatatatt 1150
tatttatTTT ttgctattta atgtatttat ttttttactt ggacatgaaa 1200
ctttaaaaaa attcacagat tatattttata acctgactag agcaggtgat 1250
gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300
ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350
gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450
ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550
ccaaaaaaaa aaaaaaaaaa a 1571

<210> 402
<211> 261
<212> PRT
<213> Homo sapiens

<400> 402
Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met
1 5 10 15
Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu
20 25 30
Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys
35 40 45
Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu
50 55 60
Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu
65 70 75
Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser
80 85 90

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr
				95					100					105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile
				110					115					120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg
				125					130					135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu
				140					145					150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys
				155					160					165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe
				170					175					180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser
				185					190					195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu
				200					205					210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys
				215					220					225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln
				230					235					240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln
				245					250					255
Trp	Met	Glu	Glu	Thr	Glu									
				260										

- <210> 403
- <211> 28
- <212> DNA
- <213> Artificial
- <220>
- <221> Artificial Sequence
- <222> 1-28
- <223> Synthetic construct.
- <400> 403
- ctcctgtggt ctccagattt caggccta 28
- <210> 404
- <211> 26
- <212> DNA
- <213> Artificial
- <220>
- <221> Artificial Sequence
- <222> 1-26
- <223> Synthetic construct.

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50
aggcttttgc cgctgacca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggtaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccgcgccat ttacagacac gtagtgtatt ctggagggtcg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tccccttttg aaatcagtca ttggagggat gatggctggt gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaattgaa 500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650
accacttatg atacagtga aactacttg gtattgaata caccacttga 700
ggacaatatc atgactcaag gtttatcaag tttatgttct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggtg agaatgacct cttggtcaat ggtgttctgg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407
<211> 31
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-31
<223> Synthetic construct.

<400> 407
cgcggtatccc gttatcgtct tgcgctactg c 31

<210> 408
<211> 34
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-34
<223> Synthetic construct.

<400> 408
gcggaattct taaaatggac tgactccact catc 34

<210> 409
<211> 1487
<212> DNA
<213> Homo sapiens

<400> 409
cggtacgcgtg ggcgcggggac gccggcaggg ttgtggcgca gcagtctcct 50
tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100
cagcatttaa tgaaaaatct atgcttaaga agtaaaaatg gcaggcttcc 150
tagataatct tcgttgcca gaattgtgaat gtattgactg gattgagaga 200
agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacaggctg 250
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300
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ataaatgctg tatccaatgc tcagggtgaga ggtgatagct atgaaagcgg 400
ctgttttagga agaacagggt ctcgagtttg gcttttcatt ggtttcatgt 450
tgatgttttg gtcacttatt gcttccatgt ggattctttt tgggtcatat 500
gttaccocaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

380

Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu
				80					85					90
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu
				95					100					105
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala
				110					115					120
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe
				125					130					135
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe
				140					145					150
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr							
				155										

<210> 411
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 411
 gtttgaggaa gctgggatac 20

<210> 412
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 412
 ccaaactcga gcacctgttc 20

<210> 413
 <211> 40
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-40
 <223> Synthetic construct.

<400> 413
 atggcaggct tcctagataa ttttcgttg ccagaatgtg 40

<210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414
gttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50
gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctggggcc 100
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcatc 350
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtggggcc 550
tactatgtgc tttgaagacc gcatgatcat gagtctgtg aaaaacaatg 600
tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950
gagatggagg gctgcatgcc cccgaagcca ttttaggggtg gctgtggctc 1000
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tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10 15
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 215 220

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-21
 <223> Synthetic construct.

 <400> 416
 gccatagtca cgacatggat g 21

 <210> 417
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 417
 ggatggccag agctgctg 18

 <210> 418
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 418
 aaagtacaag tgtggcctca tcaagc 26

 <210> 419
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 419
 tctgactcct aagtcaggca ggag 24

 <210> 420
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 420
 attctctcca cagacagctg gttc 24

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgccagga gtcgctcgc tctctctctc tctctctcac tctccctcc 200
ctctctctct gcctgtccta gtcctctagt cctcaaattc ccagtcccct 250
gcaccccttc ctgggacact atgttggtct cgcacctcct gctggagggtg 300
atttgatcc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350
acatggtcag gaccattggc cagcctotta ccctgagtgt ggaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550
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cactgggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650
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atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
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ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900
cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950
gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000
ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050
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gaagttgtat atttttgatc aatataatttg gaaattaaag tttctgactt 1700
t 1701

<210> 423

<211> 337

<212> PRT

<213> Homo sapiens

<400> 423

Met	Leu	Phe	Ser	Ala	Leu	Leu	Leu	Glu	Val	Ile	Trp	Ile	Leu	Ala
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Ala	Asp	Gly	Gly	Gln	His	Trp	Thr	Tyr	Glu	Gly	Pro	His	Gly	Gln
				20				25					30	
Asp	His	Trp	Pro	Ala	Ser	Tyr	Pro	Glu	Cys	Gly	Asn	Asn	Ala	Gln
				35				40					45	
Ser	Pro	Ile	Asp	Ile	Gln	Thr	Asp	Ser	Val	Thr	Phe	Asp	Pro	Asp
				50				55					60	
Leu	Pro	Ala	Leu	Gln	Pro	His	Gly	Tyr	Asp	Gln	Pro	Gly	Thr	Glu
				65				70					75	
Pro	Leu	Asp	Leu	His	Asn	Asn	Gly	His	Thr	Val	Gln	Leu	Ser	Leu

	80	85	90
Pro Ser Thr Leu Tyr	Leu Gly Gly Leu	Pro Arg Lys Tyr Val	Ala
95		100	105
Ala Gln Leu His	Leu His Trp Gly Gln	Lys Gly Ser Pro Gly	Gly
110		115	120
Ser Glu His Gln	Ile Asn Ser Glu Ala	Thr Phe Ala Glu Leu	His
125		130	135
Ile Val His Tyr	Asp Ser Asp Ser Tyr	Asp Ser Leu Ser Glu	Ala
140		145	150
Ala Glu Arg Pro	Gln Gly Leu Ala Val	Leu Gly Ile Leu Ile	Glu
155		160	165
Val Gly Glu Thr	Lys Asn Ile Ala Tyr	Glu His Ile Leu Ser	His
170		175	180
Leu His Glu Val	Arg His Lys Asp Gln	Lys Thr Ser Val Pro	Pro
185		190	195
Phe Asn Leu Arg	Glu Leu Leu Pro Lys	Gln Leu Gly Gln Tyr	Phe
200		205	210
Arg Tyr Asn Gly	Ser Leu Thr Thr Pro	Pro Cys Tyr Gln Ser	Val
215		220	225
Leu Trp Thr Val	Phe Tyr Arg Arg Ser	Gln Ile Ser Met Glu	Gln
230		235	240
Leu Glu Lys Leu	Gln Gly Thr Leu Phe	Ser Thr Glu Glu Glu	Pro
245		250	255
Ser Lys Leu Leu	Val Gln Asn Tyr Arg	Ala Leu Gln Pro Leu	Asn
260		265	270
Gln Arg Met Val	Phe Ala Ser Phe Ile	Gln Ala Gly Ser Ser	Tyr
275		280	285
Thr Thr Gly Glu	Met Leu Ser Leu Gly	Val Gly Ile Leu Val	Gly
290		295	300
Cys Leu Cys Leu	Leu Leu Ala Val Tyr	Phe Ile Ala Arg Lys	Ile
305		310	315
Arg Lys Lys Arg	Leu Glu Asn Arg Lys	Ser Val Val Phe Thr	Ser
320		325	330
Ala Gln Ala Thr	Thr Glu Ala		
	335		

<210> 424
 <211> 18
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
gtaaagtcgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 426
ctgcactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
cagaaaccca tgatacccta ctgaacaccg aatccccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
aattttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
acatttttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
gattctactg ttttgtcttc taggatcaac toggtcatta ccacagctca 150

aacctgcttt gggactccct cccacaaaac tggctccgga tcagggaaca 200
ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300
ctgctgcagg aatgacacct ggtacccaga cccacccatt gaccctggga 350
gggttgaatg tacaacagca actgcaccca catgtgttac caatcttctg 400
cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
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cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
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agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750
cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800
gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
tatgctgcct ggatgatatg catattaaaa catatttgga aaactggaaa 1000
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<211> 209

<212> PRT

<213> Homo sapiens

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Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
			20						25					30
Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Gln	Ser	Asn
			35						40					45
Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
			50						55					60
Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
			65						70					75

attgaagcta	taatttattt	ggaccaagga	agccctgaaa	tgaattcaac	700
aattaatatt	catgcactt	cttctgtgga	aggactttgt	gaaggaattg	750
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ccaaaaggag	atgcttctac	tggatggaat	tcagtttctc	gcatcattat	850
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tgatttcaca	ctgtttttta	atctagcatt	attcattttg	cttcaatcaa	1050
aagtggtttc	aatatttttt	ttagttgggt	agaatacttt	cttcatagtc	1100
acattctctc	aacctataat	ttggaatatt	gttggtggtc	tttggttttt	1150
ctcttagtat	agcattttta	aaaaaatata	aaagctacca	atctttgtac	1200
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Leu  Leu  Leu  Leu  Leu  Leu  Leu  Gln  Leu  Pro  Ala  Pro  Ser  Ser  Ala
      20      25      30

Ser  Glu  Ile  Pro  Lys  Gly  Lys  Gln  Lys  Ala  Gln  Leu  Arg  Gln  Arg
      35      40      45

Glu  Val  Val  Asp  Leu  Tyr  Asn  Gly  Met  Cys  Leu  Gln  Gly  Pro  Ala
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Gly  Val  Pro  Gly  Arg  Asp  Gly  Ser  Pro  Gly  Ala  Asn  Val  Ile  Pro
      65      70      75

Gly  Thr  Pro  Gly  Ile  Pro  Gly  Arg  Asp  Gly  Phe  Lys  Gly  Glu  Lys
      80      85      90

Gly  Glu  Cys  Leu  Arg  Glu  Ser  Phe  Glu  Glu  Ser  Trp  Thr  Pro  Asn
      95      100     105

Tyr  Lys  Gln  Cys  Ser  Trp  Ser  Ser  Leu  Asn  Tyr  Gly  Ile  Asp  Leu
      110     115     120

Gly  Lys  Ile  Ala  Glu  Cys  Thr  Phe  Thr  Lys  Met  Arg  Ser  Asn  Ser
      125     130     135

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Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	140	145	150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	155	160	165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	170	175	180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	185	190	195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	200	205	210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	215	220	225
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Leu Pro Lys

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